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- (71) Applicant(s)
COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION
- (72) Inventor(s)
REBECCA LOUISE HARCOURT; DANNY LLEWELLYN; JUNKO KYOZUKA; WILLIAM JAMES PEACOCK; SIMON SOUTHERTON; ELIZABETH SALISBURY DENNIS
- (74) Attorney or Agent
DAVIES COLLISON CAVE, 1 Little Collins Street, MELBOURNE VIC 3000
- (57) Claim

1. An isolated nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding a product or derivative thereof required for normal flower development in a woody perennial.

2. An isolated nucleic acid molecule according to claim 1 wherein the woody perennial is a species of the genus *Eucalyptus*.

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Name of Applicant: COMMONWEALTH SCIENTIFIC AND
INDUSTRIAL RESEARCH ORGANISATION

Actual Inventor(s): Rebecca Louise HARCOURT
William James PEACOCK
Danny LLEWELLYN
Simon SOUTHERTON
Junko KYOZUKA
Elizabeth Salisbury DENNIS

Address for Service: DAVIES COLLISON CAVE, Patent Attorneys,
1 Little Collins Street, Melbourne, 3000.

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The following statement is a full description of this invention, including the best
method of performing it known to me/us:

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ENGINEERED STERILE PLANTS AND USES THEREFOR

5 The present invention relates generally to plants and more particularly to woody perennial plants such as eucalypts with reduced reproductive capacity. The present invention is also directed to genetic constructs useful in the generation of woody perennial plants with reduced reproductive capacity. The present invention is most particularly directed to sterile trees of the genus *Eucalyptus* which are useful in the
10 establishment of wood lot plantations, in re-forestation projects and in developing modified eucalyptus trees with beneficial properties.

Bibliographic details of the publications referred to in this specification are collected at the end of the description. Sequence identity numbers (SEQ ID NOs.) for the nucleotide
15 and amino acid sequences referred to in the specification are defined after the bibliography.

Throughout this specification, unless the context requires otherwise, the word "comprise", or variations such as "comprises" or "comprising", will be understood to
20 imply the inclusion of a stated element or integer or group of elements or integers but not the exclusion of any other element or integer or group of elements or integers.

Expanding urbanisation, the agricultural industry's requirement for more arable land and the increase in demand for wood from a range of timber-related industries are
25 contributing to rapidly diminishing native forests. Despite the serious economic consequences of exhausting supply of this primary product, there are also serious environmental concerns commensurate with the loss of native forests. There is a need, therefore, to ensure adequate re-forestation and to establish wood lots of native trees in both national and regional parks and on private land holdings. There is also a need to
30 develop new varieties of native trees with beneficial properties such as resistance to pest infestation or reduced frost sensitivity.

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Although a number of reproductive genes have been isolated from plants such as *Arabidopsis* and *Antirrhinum*, until now, analogous genes had not been cloned from eucalypts. In accordance with the present invention, the inventors have cloned a number of reproductive genes involved in floral development in woody perennials such as eucalypts. The isolation and characterization of these genes will enable the generation of a series of eucalypts and other woody perennials with reduced reproductive capacity. Such plants will be useful in, for example, establishing wood lots for the timber and agricultural industries as well as in environmental planning. Furthermore, the availability of sterile eucalypts provides for the opportunity to introduce genes or other genetic sequences conferring new traits without the possibility that these traits are passed onto other trees in the event that the traits are deemed undesirable. The techniques developed in accordance with the present invention will allow the generation of a range of transgenic eucalypt trees exhibiting a variety of beneficial properties.

Accordingly, one aspect of the present invention contemplates a nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding a product or part, fragment, mutant, analogue or homologue thereof required for normal flower development in a woody perennial. For convenience, a part, fragment, mutant, analogue or homologue of the above-mentioned product is referred herein as a "derivative". Accordingly, the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding a product or derivative thereof required for normal flower development in a woody perennial.

Preferably, the woody perennial is a species of the genus *Eucalyptus*. Examples of eucalypt trees contemplated by the present invention include but are not limited to one or more of *Eucalyptus alpina*, *Eucalyptus annulata*, *Eucalyptus astringens*, *Eucalyptus behriana*, *Eucalyptus benthamii*, *Eucalyptus botryoides*, *Eucalyptus brockwayi*, *Eucalyptus caesia*, *Eucalyptus calophylla* 'Rosea', *Eucalyptus calycogona*, *Eucalyptus camaldulensis*, *Eucalyptus camaldulensis* ssp. *subcinerea*, *Eucalyptus campaspe*, *Eucalyptus camphora*, *Eucalyptus citriodora*, *Eucalyptus cladocalyx*, *Eucalyptus cladocalyx* 'Nana', *Eucalyptus cloeziana*, *Eucalyptus cornuta*, *Eucalyptus cosmophylla*,

- Eucalyptus crenulata*, *Eucalyptus crucis*, *Eucalyptus delegatensis*, *Eucalyptus desmondensis*, *Eucalyptus dielsii*, *Eucalyptus diptera*, *Eucalyptus diversicolor*, *Eucalyptus diversifolia*, *Eucalyptus dumosa*, *Eucalyptus dundasii*, *Eucalyptus dunnii*, *Eucalyptus eremophila*, *Eucalyptus erythrocorys*, *Eucalyptus erythronema*, *Eucalyptus ficifolia*,
- 5 *Eucalyptus flocktoniae*, *Eucalyptus foecunda*, *Eucalyptus forrestiana*, *Eucalyptus gardneri*, *Eucalyptus gillii*, *Eucalyptus globulus*, *Eucalyptus globulus ssp globulus*, *Eucalyptus globulus ssp. pseudoglobulus*, *Eucalyptus globulus ssp maidenii*, *Eucalyptus globulus ssp bicostata*, *Eucalyptus gomphocephala*, *Eucalyptus gracilis*, *Eucalyptus grandis*, *Eucalyptus griffithsii*, *Eucalyptus grossa*, *Eucalyptus henrii*, *Eucalyptus*
- 10 *increassata*, *Eucalyptus kitsoniana*, *Eucalyptus kondininensis*, *Eucalyptus kruseana*, *Eucalyptus lansdowneana*, *Eucalyptus largiflorens*, *Eucalyptus lehmanni*, *Eucalyptus leucoxylon*, *Eucalyptus leucoxylon (Pink) (syn. 'Rosea')*, *Eucalyptus lesouefii*, *Eucalyptus macrandra*, *Eucalyptus macrocarpa*, *Eucalyptus maculata*, *Eucalyptus marginata*, *Eucalyptus melliodora*, *Eucalyptus microcarpa*, *Eucalyptus nicholii*, *Eucalyptus nitens*,
- 15 *Eucalyptus nutans*, *Eucalyptus obliqua*, *Eucalyptus occidentalis*, *Eucalyptus ochrophloia*, *Eucalyptus oleosa*, *Eucalyptus orbifolia*, *Eucalyptus ovata*, *Eucalyptus pauciflora*, *Eucalyptus parvifolia*, *Eucalyptus perriniana*, *Eucalyptus pileata*, *Eucalyptus pellita*, *Eucalyptus pilularis*, *Eucalyptus platypus*, *Eucalyptus polyanthemus*, *Eucalyptus porosa*, *Eucalyptus preissiana*, *Eucalyptus pyriformis*, *Eucalyptus regnans*, *Eucalyptus resinifera*,
- 20 *Eucalyptus rhodantha*, *Eucalyptus robusta*, *Eucalyptus saligna*, *Eucalyptus salmonophloia*, *Eucalyptus salubris*, *Eucalyptus sargentii*, *Eucalyptus sepulcralis*, *Eucalyptus sideroxylon 'Rosea'*, *Eucalyptus sieberi*, *Eucalyptus spathulata*, *Eucalyptus socialis*, *Eucalyptus steedmanii*, *Eucalyptus stoatei*, *Eucalyptus stricklandii*, *Eucalyptus tereticornis*, *Eucalyptus tetragona*, *Eucalyptus tetraptera*, *Eucalyptus torquata*,
- 25 *Eucalyptus 'Torwood'*, *Eucalyptus urnigera*, *Eucalyptus urophylla*, *Eucalyptus viminalis*, *Eucalyptus viridis*, *Eucalyptus wandoo*, *Eucalyptus websteriana*, *Eucalyptus woodwardii*.
- The species of *Eucalyptus* may be selected from any or all of the above-listed species or from other species of *Eucalyptus* or from species related to eucalypts or which have eucalypt-like properties. Preferably, the eucalypt tree is *Eucalyptus benthamii*,
- 30 *Eucalyptus botryoides*, *Eucalyptus camaldulensis*, *Eucalyptus citriodora*, *Eucalyptus cloeziana*, *Eucalyptus delegatensis*, *Eucalyptus diversicolor*, *Eucalyptus dunnii*, *Eucalyptus globulus*, *Eucalyptus globulus subspecies bicostata*, *Eucalyptus globulus*

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subspecies *globulus*, *Eucalyptus globulus* subspecies *maidenii*, *Eucalyptus globulus* subspecies *pseudoglobulus*, *Eucalyptus grandis*, *Eucalyptus henrii*, *Eucalyptus maculata*, *Eucalyptus marginata*, *Eucalyptus nitens*, *Eucalyptus obliqua*, *Eucalyptus pellita*, *Eucalyptus pilularis*, *Eucalyptus regnans*, *Eucalyptus resinifera*, *Eucalyptus saligna*,
 5 *Eucalyptus sieberi*, *Eucalyptus tereticornis*, *Eucalyptus urophylla*, *Eucalyptus viminalis*.
 Most preferably, the eucalypt tree is *Eucalyptus globulus* ssp *globulus* or *Eucalyptus nitens*.

The nucleic acid is generally composed of deoxyribonucleotides and may be genomic
 10 DNA or cDNA. The nucleotide sequence of the nucleic acid molecule may correspond exactly with the nucleotide sequence of the naturally occurring gene or may contain one or more nucleotide substitutions, deletions and/or additions. Where the DNA is genomic DNA, the DNA may or may not contain introns.

15 In a particularly preferred embodiment, the reproductive gene is related in sequence and/or function to a corresponding gene in *Arabidopsis* and/or *Antirrhinum*.

Even more particularly, the reproductive gene corresponds to a gene selected from leafy (*LFY*), apetal 1 (*API*) or agamous (*AG*) from *Arabidopsis* or floricaula (*FLO*),
 20 squamosa (*SQUA*) or plena (*PLE*) from *Antirrhinum*.

In a most preferred embodiment, the present invention provides an isolated DNA molecule selected from the following:

- 25 (i) having a sequence set forth in SEQ ID NO:1 or 3 or 5 and analogous to *LFY* and/or *FLO*;
- (ii) having a sequence set forth in SEQ ID NO:9 or 11 or 13 and analogous to *API* and/or *SQUA*; or
- (iii) having a sequence set forth in SEQ ID NO:7 or 15 and analogous to *AG* and/or
 30 *PLE*.

The eucalypt genes defined in (i), (ii) and (iii) above are referred to herein as *FLE*, *SQE* and *AGE*, respectively.

- 5 According to preferred embodiments of the present invention, there is provided in one aspect, a DNA molecule of eucalypt origin encoding a reproductive gene and capable of hybridizing under low stringency conditions to a nucleic acid molecule having a nucleotide sequence as set forth in or complementary to SEQ ID NO:1 or 3 or 5.
- 10 In another aspect, there is provided a DNA molecule of eucalypt origin encoding a reproductive gene and capable of hybridizing under low stringency conditions to a nucleic acid molecule having a nucleotide sequence as set forth in or complementary to SEQ ID NO:9 or 11 or 13.
- 15 In still another aspect, there is provided a DNA molecule of eucalypt origin encoding a reproductive gene and capable of hybridizing under low stringency conditions to a nucleic acid molecule having a nucleotide sequence as set forth in or complementary to SEQ ID NO:7 or 15.
- 20 For the purposes of defining the level of stringency, reference can conveniently be made to Sambrook *et al* (1989) which is herein incorporated by reference where the washing steps at pages 9.52-9.57 are considered high stringency. A low stringency is defined herein as being in 0.1-0.5% w/v SDS at 37-45°C for 2-3 hours. Depending on the source and concentration of nucleic acid involved in the hybridisation, alternative
- 25 conditions of stringency may be employed such as medium stringent conditions which are considered herein to be 0.25%-0.5% w/v SDS at $\geq 45^{\circ}\text{C}$ for 2-3 hours or high stringent conditions as disclosed by Sambrook *et al* (1989).

- In an alternative embodiment, the preferred nucleic acid molecule of the present
- 30 invention comprises a nucleotide sequence having at least about 45%, more preferably at least about 55%, still more preferably at least about 65%, yet still more preferably at least about 75-80% and even still more preferably at least about 85-95% nucleotide

similarity to at least one of SEQ ID NO:1 or 3 or 5, SEQ ID NO:9 or 11 or 13 or SEQ ID NO:7 or 15.

The present invention also contemplates a method for identifying a gene required for normal flower development in a woody perennial, said method comprising isolating a nucleic acid molecule from said woody perennial and cloning a region of said nucleic acid molecule having at least 45% nucleotide similarity to all or a region of *Arabidopsis* genes *LFY*, *API* or *AG* or *Antirrhinum* genes *FLO*, *SQUA* or *PLE*.

10 Preferably, the woody perennial is a species of the genus *Eucalyptus* such as *Eucalyptus benthamii*, *Eucalyptus botryoides*, *Eucalyptus camaldulensis*, *Eucalyptus citriodora*, *Eucalyptus cloeziana*, *Eucalyptus delegatensis*, *Eucalyptus diversicolor*, *Eucalyptus dunnii*, *Eucalyptus globulus*, *Eucalyptus globulus* subspecies *bicostata*, *Eucalyptus globulus* subspecies *globulus*, *Eucalyptus globulus* subspecies *maidenii*, *Eucalyptus globulus* subspecies *pseudoglobulus*, *Eucalyptus grandis*, *Eucalyptus henrii*, *Eucalyptus maculata*, *Eucalyptus marginata*, *Eucalyptus nitens*, *Eucalyptus obliqua*, *Eucalyptus pellita*, *Eucalyptus pilularis*, *Eucalyptus regnans*, *Eucalyptus resinifera*, *Eucalyptus saligna*, *Eucalyptus sieberi*, *Eucalyptus tereticornis*, *Eucalyptus urophylla*, *Eucalyptus viminalis*. Most preferably, the species is *Eucalyptus globulus ssp globulus* or
15 *Eucalyptus nitens*.
20

The nucleic acid molecules of the present invention are useful for generating antisense or ribozyme molecules or overexpression of sense molecules using a constitutive promoter or in co-suppression of the subject reproductive genes. By targeting such genes, their expression is diminished, reduced or otherwise lowered to levels which result in reproductive sterility or at least substantially reduced reproductive capacity.

According to one embodiment there is provided a nucleic acid molecule comprising at least 5 contiguous nucleotide bases capable of hybridizing to, forming a duplex with or otherwise reducing translation of target reproductive gene-specified mRNA. This embodiment of the present invention defines primers, probes and other antisense molecules capable of instituting or at least reducing translation of the reproductive gene-

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specified mRNA. Although the preferred antisense molecules are at least about 10 to 20 nucleotides in length, the present invention extends to molecules of 50-100 nucleotide bases in length or a molecule corresponding to a full length or substantially full length reproductive gene-specified mRNA.

5

Co-suppression involves introducing a second copy of an endogenous gene or a substantially similar copy or analogue of an endogenous gene. Over expression involves introducing a second copy of an endogenous gene or a substantially similar copy or analogue of an endogenous gene fused to a constitutive promoter.

10

Ribozymes are synthetic RNA molecules which possess highly specific endoribonuclease activity. In particular, they comprise a hybridizing region which is complementary in nucleotide sequence to at least part of a target RNA. Ribozymes are well described by Haseloff and Gerlach (1988) and in International Patent Application No. WO 89/05852.

15

The present invention extends to ribozymes which target reproductive gene mRNA.

20

According to this embodiment, there is provided a ribozyme comprising a hybridizing region and a catalytic region wherein the hybridizing region is capable of hybridizing to at least part of a target mRNA sequence transcribed from a reproductive gene and more particularly as defined by SEQ ID NO:1 or 3 or 5, SEQ ID NO:9 or 11 or 13 or SEQ ID NO:7 or 15, wherein said catalytic domain is capable of cleaving said target mRNA sequence to reduce or substantially inhibit reproductive capacity in a woody perennial and more particularly a eucalypt.

25

The present invention extends to genetic constructs designed to facilitate expression of the antisense molecule, co-suppression molecule, overexpression molecule or ribozyme.

30

Generally, the genetic construct comprises in addition to the subject nucleic acid molecule, a promoter and optionally other regulatory sequences to facilitate expression of the nucleic acid molecule. The promoter may be derived from a genomic clone encoding the reproductive gene or may be a heterologous promoter from another source. Preferably, however, the promoter is tissue specific capable of expression substantially only in reproductive tissue for antisense, ribozyme and co-suppression molecules. For

Yet another aspect of the present invention contemplates a method of minimising inflorescence in a woody perennial such as a eucalypt, said method comprising introducing into one or more cells of said woody perennial a genetic construct capable of down regulating expression of a reproductive gene in said woody perennial.
5 regenerating a transgenic plant from said one or more cells and growing said plant for a time and under conditions sufficient to permit expression of said genetic construct.

Preferably, the woody perennial is a eucalypt, such as selected from the previously mentioned list. Preferably, the eucalyptus is *Eucalyptus benthamii*, *Eucalyptus botryoides*, *Eucalyptus camaldulensis*, *Eucalyptus citriodora*, *Eucalyptus cloeziana*, *Eucalyptus delegatensis*, *Eucalyptus diversicolor*, *Eucalyptus dunnii*, *Eucalyptus globulus*, *Eucalyptus globulus subspecies globulus*, *Eucalyptus globulus subspecies bicostata*, *Eucalyptus globulus subspecies maidenii*, *Eucalyptus globulus subspecies pseudoglobulus*, *Eucalyptus grandis*, *Eucalyptus henrii*, *Eucalyptus maculata*, *Eucalyptus marginata*, *Eucalyptus nitens*, *Eucalyptus obliqua*, *Eucalyptus pellita*, *Eucalyptus pilularis*, *Eucalyptus regnans*, *Eucalyptus resinifera*, *Eucalyptus saligna*, *Eucalyptus sieberi*, *Eucalyptus tereticornis*, *Eucalyptus urophylla*, *Eucalyptus viminalis*. Most preferably the eucalypt is *Eucalyptus globulus ssp globulus* or *Eucalyptus nitens*.
15

20 Preferably, the reproduction gene corresponds to one or more of SEQ ID NO:1 or 3 or 5, SEQ ID NO:9 or 11 or 13 or SEQ ID NO:7 or 15.

Preferably, the transgenic plant exhibits a substantial reduction in reproductive capability. More preferably, the plant is substantially sterile.

25

Still yet a further aspect of the present invention is directed to a transgenic eucalypt plant such as a eucalypt selected from the previously mentioned list wherein the plant exhibits substantially reduced reproductive sterility.

The present invention is further described by the following non-limiting Figures and/or Examples.

5 In the Figures:

Figure 1 is a representation of the nucleotide sequence of genomic clone *FLE2* with the predicted amino acid sequences. The positions of the PCR primers used to isolate the gene are underlined.

10

Figure 2 is a representation of the nucleotide sequence of *AGE1* cDNA with its predicted amino acid sequence. The MADS box and position of the PCR primers used to isolate the gene are underlined.

15 Figure 3 is a representation of the nucleotide sequence of *SQE1* cDNA. The MADS box is underlined; the amino acids at the positions of the PCR primers used to isolate the gene are in italics.

Figure 4 is a representation of the nucleotide sequence of *SQE2S* cDNA with its predicted amino acid sequence. The MADS box is single underlined; the amino acids at the positions of the PCR primers used to isolate the genes are double underlined.

20

Figure 5 is a representation of the nucleotide sequence of *SQE2L* cDNA with its predicted amino acid sequence. The MADS box is single underlined; the amino acids at the positions of the PCR primers used to isolate the genes are double underlined.

25

Figure 6 is a representation of nucleotide sequence of *AGE2* with its predicted amino acid sequence. The MADS box is single underlined; the amino acids at the positions of the PCR primers used to isolate the genes are double underlined.

30

Single and three letter abbreviations used for amino acid residues in the specification are defined in Table 1.

5

TABLE 1

	Amino Acid	Three-letter Abbreviation	One-letter
			Symbol
10	Alanine	Ala	A
	Arginine	Arg	R
	Asparagine	Asn	N
	Aspartic acid	Asp	D
	Cysteine	Cys	C
15	Glutamine	Gln	Q
	Glutamic acid	Glu	E
	Glycine	Gly	G
	Histidine	His	H
	Isoleucine	Ile	I
20	Leucine	Leu	L
	Lysine	Lys	K
	Methionine	Met	M
	Phenylalanine	Phe	F
	Proline	Pro	P
25	Serine	Ser	S
	Threonine	Thr	T
	Tryptophan	Trp	W
	Tyrosine	Tyr	Y
	Valine	Vai	V
30.			

A summary of SEQ ID NOs used throughout the specification is shown in Table 2.

TABLE 2

5

SEQ ID NO	DEFINITION
SEQ ID NO:1	Genomic clone of <i>FLE</i>
10 SEQ ID NO:2	Predicted amino acid sequence of <i>FLE</i> -1
SEQ ID NO:3	Genomic clone of <i>FLE</i>
SEQ ID NO:4	Predicted amino acid sequence of <i>FLE</i> -2
SEQ ID NO:5	Genomic clone of <i>FLE</i>
SEQ ID NO:6	Predicted amino acid sequence of <i>FLE</i> -3
15 SEQ ID NO:7	cDNA <i>AGE</i> 1 clone
SEQ ID NO:8	Predicted amino acid sequence of <i>AGE</i> 1
SEQ ID NO:9	cDNA <i>SQE</i> 1 clone
SEQ ID NO:10	Predicted amino acid sequence of <i>SQE</i> 1
SEQ ID NO:11	cDNA <i>SQE</i> 2S clone
20 SEQ ID NO:12	Predicted amino acid sequence of <i>SQE</i> 2S
SEQ ID NO:13	cDNA <i>SQE</i> 2L clone
SEQ ID NO:14	Predicted amino acid sequence of <i>SQE</i> 2L
SEQ ID NO:15	cDNA <i>AGE</i> 2 clone
25 SEQ ID NO:16	Predicted amino acid sequence of <i>AGE</i> 2

Identification *Arabidopsis* and *Antirrhinum* genes and the names of eucalypt homologues are shown in Table 3.

5 **TABLE 3**

	<i>Arabidopsis</i>	<i>Antirrhinum</i>	<i>Eucalyptus</i>
10	Leafy (<i>LFY</i>)	Floricaula (<i>FLO</i>)	<i>FLE</i>
	Apetala 1 (<i>API</i>)	Squamosa (<i>SQUA</i>)	<i>SQE</i>
	Agamous (<i>AG</i>)	Plena (<i>PLE</i>)	<i>AGE</i>

15 **EXAMPLE 1**

Isolation of the eucalypt genes

The strategy used to isolate the eucalypt genes involved design and synthesis of polymerase chain reaction (PCR) primers to regions of amino acid homology between
 20 the *Arabidopsis* and *Antirrhinum* genes. These primers were then used to amplify from eucalypt DNA (*FLE*) or cDNA (*AGE* and *SQE*) short regions of DNA from the eucalypt homologue. The DNA fragments obtained were then used as probes to screen *Eucalyptus globulus* libraries to obtain the full length genes.

25 **EXAMPLE 2**

FLE

Three copies of *FLE* were isolated from a *Eucalyptus globulus* genomic library. Two of these copies were not functional because the sequences were interrupted by stop
 30 codons and frame shifts. These two copies were found to be two alleles at a pseudogene locus. The other copy appears to be the homologue of the *LFY* and *FLO* genes in eucalypts. The predicted protein product of *FLE2* is 359 amino acids in length and

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shares 67% identical aa with *LFY* and 71% identical aa with *FLO*. The nucleotide sequence (SEQ ID NO:1) and the predicted amino acid sequences (SEQ ID NO:2, 4 and 6) of the genomic clone of *FLE2* are shown in Figure 1.

5 Expression of *FLE2* RNA was determined by in situ hybridization. *FLE2* RNA was observed in developing floral organs in a similar manner to the expression patterns of *FLORICAULA* and *LEAFY*. In addition, *FLE2* is strongly expressed in the primordia of true leaves as they develop on the flanks of apical and lateral vegetative meristems. Expression was not detected in the centre of the vegetative apical meristem or in stems
10 or roots. Its observed expression in vegetative and floral tissue possibly suggests a wider role for this gene in *Eucalyptus* development.

The promoter of the *FLE2* gene was also isolated from the genomic library. One kilobase (kb) of the promoter has been sequenced and 2 kb have been used in sterility
15 constructs.

EXAMPLE 3

AGE1 and *AGE2*

20 Full length cDNA clones of *AGE1* were isolated from a cDNA library constructed from RNA from mature flower buds. The gene encodes a protein which is 251 amino acids in length with amino acid homology between the *AGE1* protein and the *AG* protein of about 68% and with the *PLE* protein, about 75%. The *AG* and *PLE* proteins contain a conserved region of 56 amino acids known as the MADS box region. This region is
25 present in a number of different genes involved in floral development. The *AGE1* gene also contains this region of 56 amino acids which is identical to that of the *AG* MADS box. Two of the 56 amino acids differ between *PLE* and *AGE1*. Southern blots of *Eucalyptus globulus* DNA probed with a fragment of *AGE1* cDNA which does not contain the MADS box suggest that there is only one copy of the *AGE1* gene in the
30 eucalypt genome. The nucleotide sequence of the *AGE1* cDNA and the predicted amino acid sequence are shown in Figure 2. The nucleotide sequence of another cDNA clone, *AGE2*, is shown in Figure 6 with its predicted amino acid sequence. *AGE2* is 229

- 15 -

amino acids in length. It has good homology to both the AG and PLE proteins, of 62% and 64%, respectively.

The fact that both *AGE1* and *AGE2* were isolated from a cDNA library is a good indication that these genes are functional. An RNA probe made from *AGE1* was used to screen RNA isolated from mature, medium and young flower buds, anthers, leaves, stems and roots of *Eucalyptus globulus*. The hybridisation pattern suggests that *AGE* is expressed very highly in mature flower buds and not at all in leaves, stems or roots. The level of expression in anthers and medium flower buds is moderate. There is very low, if any, expression in young flower buds. This pattern of expression is very similar to that of *AG* and *PLE*. *AGE2*, however, is strongly expressed only in anthers, young flower buds and mature flower buds. It is weakly expressed in leaves.

In order to isolate the *AGE* promoter, an *Eucalyptus globulus* genomic DNA library was screened with a fragment of *AGE* cDNA that does not contain the MADS region to avoid cross-hybridisation with other MADS-containing genes. A number of clones have been identified. The promoter is used to generate a series of sterility constructs in *Arabidopsis* and *Eucalyptus*.

20

EXAMPLE 4 *SQE1* and *SQE2*

The fragment of the *SQE1* and *SQE2* genes amplified from cDNA was from within the MADS box. When a cDNA library constructed from RNA from young flower buds was screened with this probe, four clones were isolated. One of these genes, *SQE1*, contains a MADS box with 95% homology to *API* and 91% homology to *SQUA*. Sequencing of the gene has revealed 69% homology to *API* at the DNA level. The DNA sequence and predicted amino acid sequence of *SQE1* are shown in Figure 3. Other genes isolated are designated *SQE2S* having a DNA sequence and predicted amino acid sequence shown in Figure 4 (SEQ ID NOs 11 and 12, respectively) and *SQE2L* having a DNA sequence and predicted amino acid sequence shown in Figure 5 (SEQ ID NOs 13 and 14, respectively). These genes will be investigated for their potential for use in the

sterility strategy.

The promoters of the genes may be used to generate sterility constructs.

5

EXAMPLE 5

Ectopic Expression of the Eucalypt genes in *Arabidopsis* confirms their functional similarity to the *Arabidopsis* genes

To examine the function of the two genes in flower development, *AGE1* and *AGE2*
10 cDNAs were ectopically expressed (also known as overexpression) in *Arabidopsis* plants
under the control of the cauliflower mosaic virus 35S promoter. More than 60
independent transgenic plants were regenerated for each construct. The most commonly
observed phenotype in the primary transformants was that the sepals developed stigmatic
papillae, the petals became staminoid or were shorter than normal while the stamens and
15 carpels appeared normal or occasionally the carpels were unfused. Most of the plants,
however, were sterile. 25% of 35S-*AGE1* and 29% of 35S-*AGE2* transformants showed
this phenotype. Some plants showed a severe phenotype while others showed a weaker
one. As most plants were sterile it was impossible to test the segregation of the
transgene in the next generation. Of the plants that were fertile, most appeared to
20 produce a normal phenotype in the next generation, suggesting that there was very weak
expression of the gene. Based on the phenotype of the primary transformants it appears
that (1) both the *AGE1* and *AGE2* genes from *Eucalyptus* are functional in *Arabidopsis*;
(2) that they have a similar function to the *AG* gene of *Arabidopsis*; and (3) high levels
of expression of either or both the *AGE1* and *AGE2* genes in transgenic *Eucalyptus* may
25 lead to sterile plants. Thus, expression of flowering genes using the CaMV35S promoter
to cause disruption of flowering is an alternative strategy to that of antisense, co-
suppression or RNase genes.

To examine the function of the two eucalypt genes (*SQE1* and *SQE2L*) in flower
30 development, and the *Arabidopsis* gene, *API*, the three cDNAs were ectopically
expressed in *Arabidopsis* plants under the control of the CaMV35S promoter. More than
50 independent transgenic plants were regenerated for each construct. The most

commonly observed phenotype in the primary transformants was a homeotic conversion of stem meristems into flowers - these plants resembled the *Arabidopsis* mutant *terminal flower* (*tfl*). Development of the stem meristem, which is normally indeterminate, stops early in transgenic plants with a severe *tfl*-like phenotype. Instead they form an abnormal flower at the top of the stems. The terminal flower consists of the disorganised aggregation of many floral organs. 30%, 43% and 30% of the transformed plants carrying 35S-*AP1*, 35S-*SQE1* and 35S-*SQE2L*, respectively, showed the *tfl*-like phenotype. Although the severity and the details of the phenotype varied between independent transgenic plants, the overall ranges of phenotypes observed seemed to be similar between the three different constructs.

The phenotype was analysed in detail in the T_1 generation grown on soil. The *tfl*-like phenotype observed in the T_0 generation was inherited in the next generation as a dominant Mendelian trait and it co-segregated with kanamycin resistance. Table 4 summarises the characteristics of six independent transgenic lines. T_1 transgenic plants flowered earlier compared to control plants. They formed an increased number of stems and were shorter than control plants.

These results indicate that the *Eucalyptus* genes, *SQE1* and *SQE2L* have the same function as the *Arabidopsis AP1* gene in flower development.

TABLE 4

Comparison of flowering time, number of stems and height of main stem in transgenic (T₁) and wild type (C24) *Arabidopsis* plants.

	Transgenic line	Days to flowering	Number of stems	Height of main stem (cm)
35S-AP1	A15	17.0	2.0	5.2
	A52	14.0	3.0	3.5
35S-SQE1	S1-23	16.0	5.5	2.5
	S1-25	13.0	4.6	2.0
35S-SQE2L	S2-16	12.0	1.8	2.3
	S2-28	13.5	5.3	2.4
Control		19.7	1.2	18.8

EXAMPLE 5

Genetic Constructs Conferring Sterility : *in vivo*
model using *Arabidopsis*

A number of constructs are tested for their ability to prevent flowering in *Arabidopsis* (Table 5). Constructs are transformed into wild-type *Arabidopsis* and plants regenerated. One plant, from construct 1, independent transgenic line 1, had a phenotype very similar to that of the LEAFY mutant which exhibits female-fertility but is completely male sterile. This result strongly indicates that an antisense approach is capable of mimicking the mutant phenotypes observed in *Arabidopsis*. This plant was cross-pollinated and a small number of seeds collected for further analysis. One other plant from construct 1 had a similar but less pronounced phenotype. Plants from all other lines of construct 1 and the other constructs have been allowed to self-pollinate, seed from the T₀ plants

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has been collected and planted out in soil. Seed of seven independent (T0) transgenic lines were planted out from construct 1. One line (1-17) showed several plants (T1) with an altered phenotype. The T0 plant that produced this seed appeared normal. One of the eleven plants from this line (1-17) has a phenotype very similar to that of the strongest allele of the *LEAFY* mutant which is male-sterile with very much reduced female fertility. Nine plants have phenotypes similar to the mutants of the weaker alleles of *LEAFY*. These eleven plants will be further analysed. These results strongly support the hypothesis that we can produce sterile plants by introducing antisense to these genes into transgenic plants.

10

Sterility constructs are made with antisense to *LEAFY*, *API* and both *LEAFY* and *API* in the one construct. These antisense constructs are expressed by the histone promoter H4A or the CaMV35S promoter which has been observed to give high expression in young flower buds.

15

TABLE 5

Constructs tested in *Arabidopsis* and the number of transformed plants obtained.

20

Promoter	Gene	Number of plants obtained
25 1. leafy	antisense leafy	52
2. leafy	antisense <i>AG-MADS</i>	84
3. 35S	antisense leafy	30
4. FLE2	antisense FLE2	50

30

- 20 -

Those skilled in the art will appreciate that the invention described herein is susceptible to variations and modifications other than those specifically described. It is to be understood that the invention includes all such variations and modifications. The
5 invention also includes all of the steps, features, compositions and compounds referred to or indicated in this specification, individually or collectively, and any and all combinations of any two or more of said steps or features.

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REFERENCES:

Hase' Perlach L., *Nature* 334: 586-594, 1988

Samb. et al, *Molecular Cloning : A Laboratory Manual*, Cold Spring Harbour Laboratory, Cold Spring Harbour, New York, USA, 1989

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: COMMONWEALTH SCIENTIFIC AND
INDUSTRIAL RESEARCH ORGANISATION
INVENTORS: HARCOURT, R., KYOZUKA, J., DENNIS, E.,
PEACOCK, W.J., SOUTHERTON, S. and
LLEWELLYN, D.
- (ii) TITLE OF INVENTION: ENGINEERED STERILE PLANTS AND USES
THEREFOR
- (iii) NUMBER OF SEQUENCES: 16
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: DAVIES COLLISON CAVE
 - (B) STREET: 1 LITTLE COLLINS STREET
 - (C) CITY: MELBOURNE
 - (D) STATE: VICTORIA
 - (E) COUNTRY: AUSTRALIA
 - (F) ZIP: 3000
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: AU COMPLETE
 - (B) FILING DATE: 21-NOV-1995
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PM9589
 - (B) FILING DATE: 22-NOV-1994
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: HUGHES, DR E JOHN L
 - (C) REFERENCE/DOCKET NUMBER: EJH/EK
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: +61 3 9254 2777
 - (B) TELEFAX: +61 3 9254 2770
 - (C) TELEX: AA31787

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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1500 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 121..453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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CCACTACGTA CGTACATACA GTGTACATTG AATATACTAA ACAGATGGAC CCATGTGTTT      60
ATAAAACAAG GAAGCGAGAG TCCTGTACCC TTACACGCTG AAGCCATTG AAGCGCCAGA      120
ATG GAT CCA GAA GCA TTT GCG GTT GTG GGG TTG CGA ACG ATG GGG GGA      168
Met Asp Pro Glu Ala Phe Ala Val Val Gly Leu Arg Thr Met Gly Gly
  1           5           10           15
CTG GAG GAG CTG TTC GAG GCT TAT GGC ATA AGG TAC CTC ACG GCC TCC      216
Leu Glu Glu Leu Phe Glu Ala Tyr Gly Ile Arg Tyr Leu Thr Ala Ser
  20           25           30
AGG ATA GCG GAA ATG GGG TTT ACG GCC AAC ACC CTC CTC GAC ATG AAG      264
Arg Ile Ala Glu Met Gly Phe Thr Ala Asn Thr Leu Leu Asp Met Lys
  35           40           45
GAG GAG GAG CTC GAC GAC ATG ATG AAC TCC CTC TCC CAC ATC TTC CGC      312
Glu Glu Glu Leu Asp Asp Met Met Asn Ser Leu Ser His Ile Phe Arg
  50           55           60
TGG GAC CTC CTC GTC GGC GAG CGC TAC GGC ATC AAG GCC GCC ATC CGC      360
Trp Asp Leu Leu Val Gly Glu Arg Tyr Gly Ile Lys Ala Ala Ile Arg
  65           70           75           80
GCC GAG CGC CGA CGC CTC CTC GAA GCC GAT GAC CGC CGC CAC CAC CTC      408
Ala Glu Arg Arg Arg Leu Leu Glu Ala Asp Asp Arg Arg His His Leu
  85           90           95
CAC TCC ACC GAC CAT GCC CTC CTC GAT GCT CTC TCC CAC CAA GGT      453
His Ser Thr Asp His Ala Leu Leu Asp Ala Leu Ser His Gln Gly
  100          105          110
ACCTTAGCTC GGCCTCTTTG ATTTTGGACG TTTTGGGTCA TTATGATTAT TCCCACGCAG      513
GGCTGTCCGA GGAACAAGTG GTGCAGCACT CAGAGAAGGA TCAGCTGGGC AGGCGGGGAA      573
GCGGGGACAC GGCGGGCACG TCGTGGGGCG CCCAACAACA GAGAAAGAAG CATCGTCATC      633
GTCACCACAT CACCGCGATG AAAGGAGCGG CCACGGAAGA GGACGAGGAG GACGAGGAGG      693
AAGTGGAGGA GATGAGGAGG CAGAGGGAGC ACCCCTTCAT AGTGACGGAG CCCGGGGAGG      753
TGGCGCGTGG GAAGAAGAAC GGCCTGGACT ACCTCTTCCA TCTCTACGAC CAGTGCCGCG      813
ACTTCCTCCT CCAAGTCAA TCCTTGGCCA AGGAGCGGGG CGAGAAATGC CCCACCAAGG      873
TCCTCCGCCT CTCTTCTTTT TATAGTCTTT CGATACAATC AAACCTCTTC GAACGTACCC      933

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AAGCACGGAT CATTCAAACA AGAAGACAAT GCAGGTGACG AACCAGGTGT TCAGGTACGC 993
 GAAGAAGGCG GGAGCAAGCT ACATAAACAA GCCGAAGATG AGGCACTATG TCCACTGCTA 1053
 CGCCCTGCAC TGCCTGGACG AGCACGCCTC CAACGCCCTT CGCAAGAGCT TCAAGGAGCG 1113
 CGGGGAGAAC GTCGGCGCCT GGAGGCAAGC CTGTTACCAC CCCCTGGTCA CCATCGCCGG 1173
 CCGCAGGGCC GGCTGGGACA TCGACGCCAT CTTCAATGCC CACCCCGCC TCTGCATCTG 1233
 GTATGTCCCC ACCAAGCTCC GCCAGCTCTG CCATGCTCAC CGCCACTCCT CCGCCTCTGC 1293
 TGCTTCTCC GCTTCCACCT CCACCTCTCC CCCCACCGCT CACCATCTCG AACTCCCTTA 1353
 CTAGTTCTGC CCCGTTCTCT ATTCTCTTGT GTTTTAGTGT CGTATCAGCG CATGATCATG 1413
 AGGGAGATGA AAGTACTGTG CTGTGGTCTA TTTCTACTGC AATGAGTATA AATTGAATTT 1473
 TAACGTGTAG CTGAGCTGAG CTGAGCT 1500

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Pro Glu Ala Phe Ala Val Val Gly Leu Arg Thr Met Gly Gly
 1 5 10 15
 Leu Glu Glu Leu Phe Glu Ala Tyr Gly Ile Arg Tyr Leu Thr Ala Ser
 20 25 30
 Arg Ile Ala Glu Met Gly Phe Thr Ala Asn Thr Leu Leu Asp Met Lys
 35 40 45
 Glu Glu Glu Leu Asp Asp Met Met Asn Ser Leu Ser His Ile Phe Arg
 50 55 60
 Trp Asp Leu Leu Val Gly Glu Arg Tyr Gly Ile Lys Ala Ala Ile Arg
 65 70 75 80
 Ala Glu Arg Arg Arg Leu Leu Glu Ala Asp Asp Arg Arg His His Leu
 85 90 95
 His Ser Thr Asp His Ala Leu Leu Asp Ala Leu Ser His Gln Gly
 100 105 110

- 25 -

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1500 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 516..872

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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ATGGATCCAG AAGCATTGTC GGTTGTGGGG TTGCGAACGA TGGGGGGACT GGAGGAGCTG      180
TTCGAGGCTT ATGGCATAAG GTACCTCAGC GCCTCCAGGA TAGCGGAAAT GGGGTTTACG      240
GCCAACACCC TCCTCGACAT GAAGGAGGAG GAGCTCGACG ACATGATGAA CTCCTCTCTC      300
CACATCTTCC GCTGGGACCT CCTCGTCGGC GAGCGCTACG GCATCAAAGC CGCCATCCGC      360
GCCGAGCGCC GACGCCTCCT CGAAGCCGAT GACCGCCGCC ACCACCTCCA CTCCACCGAC      420
CATGCCCTCC TCGATGCTCT CTCCCACCAA GGTACCTTAG CTCGGCCTCT TTGATTTTGT      480
ACGTTTTGGG TCATTATGAT TATTCCCACG CAGGG CTG TCG GAG GAA CAA GTG      533
                               Leu Ser Glu Glu Gln Val
                               1           5

GTG CAG CAC TCA GAG AAG GAT CAG CTG GGC AGG GCG GGA AGC GGG GAC      581
Val Gln His Ser Glu Lys Asp Gln Leu Gly Arg Ala Gly Ser Gly Asp
          10           15           20

ACG GCG GGC ACG TCG TGG GGC GCC CAA CAA CAG AGA AAG AAG CAT CGT      629
Thr Ala Gly Thr Ser Trp Gly Ala Gln Gln Gln Arg Lys Lys His Arg
          25           30           35

CAT CGT CAC CAC ATC ACC GCG ATG AAA GGA GCG GCC ACG GAA GAG GAC      677
His Arg His His Ile Thr Ala Met Lys Gly Ala Ala Thr Glu Glu Asp
          40           45           50

GAG GAG GAC GAG GAG GAA GTG GAG GAG ATG AGG AGG CAG AGG GAG CAC      725
Glu Glu Asp Glu Glu Glu Val Glu Glu Met Arg Arg Gln Arg Glu His
          55           60           65           70

CCC TTC ATA GTG ACG GAG CCC GGG GAG GTG GCG CGT GGG AAG AAG AAC      773
Pro Phe Ile Val Thr Glu Pro Gly Glu Val Ala Arg Gly Lys Lys Asn
          75           80           85

GGC CTG GAC TAC CTC TTC CAT CTC TAC GAC CAG TGC CGC GAC TTC CTC      821
Gly Leu Asp Tyr Leu Phe His Leu Tyr Asp Gln Cys Arg Asp Phe Leu
          90           95           100

CTC CAA GTC CAA TCC TIG GCC AAG GAG CGG GGC GAG AAA TGC CCC ACC      869
Leu Gln Val Gln Ser Leu Ala Lys Glu Arg Gly Glu Lys Cys Pro Thr
          105           110           115

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AAG GTCCTCCGCC ACTCTCTTT TTATAGTCTT TCGATACAAT CAAACTTCTT 922
 Lys

CGAACGTACC CAAGCACGGA TCATTCAAAC AATAGACAA TGCAGGTGAC GAACCAGGTG 982
 TTCAGGTACG CGAAGAAGGC GGGAGCAAGC TACATAAACA AGCCGAAGAT GAGGCACTAT 1042
 GTCCACTGCT ACGCCCTGCA CTGCCTGGAC GAGCACGCCT CCAACGCCCT TCGCAAGAGC 1102
 TTCAAGGAGC GCGGGGAGAA CGTCGGCGCC TGGAGGCAAG CCTGTTACCA CCCCCTGGTC 1162
 ACCATCGCCG GCCGCAGGGC CGGCTGGGAC ATCGACGCCA TCTTCAATGC CCACCCCCGC 1222
 CTCTGCATCT GGTATGTCCC CACCAAGCTC CGCCAGCTCT GCCATGCTCA CCGCCACTCC 1282
 TCCGCCTCTG CTGCTTCCTC CGCTTCCACC TCCACCTCTG CCCCCACCGC TCACCATCTC 1342
 GAACTCCCTT ACTAGTTCGT GCCCGTTCCT CATTCTCTTG TGTTTTAGTG TCGTATCAGC 1402
 GCATGATCAT GAGGGAGATG AAAGTACTGT GCTGTGGTCT ATTTCTACTG CAATGAGTAT 1462
 TAATTGAATT TTAACGTGTA GCTGAGCTGA GCTGAGCT 1500

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu Ser Glu Glu Gln Val Val Gln His Ser Glu Lys Asp Gln Leu Gly
 1 5 10 15

Arg Ala Gly Ser Gly Asp Thr Ala Gly Thr Ser Trp Gly Ala Gln Gln
 20 25 30

Gln Arg Lys Lys His Arg His Arg His His Ile Thr Ala Met Lys Gly
 35 40 45

Ala Ala Thr Glu Glu Asp Glu Glu Asp Glu Glu Glu Val Glu Glu Met
 50 55 60

Arg Arg Gln Arg Glu His Pro Phe Ile Val Thr Glu Pro Gly Glu Val
 65 70 75 80

Ala Arg Gly Lys Lys Asn Gly Leu Asp Tyr Leu Phe His Leu Tyr Asp
 85 90 95

Gln Cys Arg Asp Phe Leu Leu Gln Val Gln Ser Leu Ala Lys Glu Arg
 100 105 110

Gly Glu Lys Cys Pro Thr Lys
 115

- 27 -

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1500 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 968..1354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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ATGGATCCAG AAGCATTGTC GGTGTGTTGGG TTGCGAACGA TGGGGGGACT GGAGGAGCTG      180
TTCGAGGCTT ATGGCATAAG GTACCTCACG GCCTCCAGGA TAGCGGAAAT GGGGTTTACG      240
GCCAACACCC TCCTCGACAT GAAGGAGGAG GAGCTCGACG ACATGATGAA CTCCTCTCTC      300
CACATCTTCC GCTGGGACCT CCTCGTCGGC GAGCGCTACG GCATCAAGGC CGCCATCCGC      360
GCCGAGCGCC GACGCCTCCT CGAAGCCGAT GACCGCCGCC ACCACCTCCA CTCCACCGAC      420
CATGCCCTCC TCGATGCTCT CTCCCACCAA GGTACCTTAG CTCGGCCTCT TTGATTTTGT      480
ACGTTTTTGGG TCATTATGAT TATTCCCACG CAGGGCTGTC GGAGGAACAA GTGGTGACGC      540
ACTCAGAGAA GGATCAGCTG GGCAGGGCGG GAAGCGGGGA CACGGCGGGC ACGTCGTGGG      600
GCGCCCAACA ACAGAGAAAG AAGCATCGTC ATCGTCACCA CATCACC CG ATGAAAGGAG      660
CGGCCACGGA AGAGGACGAG GAGGACGAGG AGGAAGTGA GGAGATGAGG AGGCAGAGGG      720
AGCACCCCTT CATAGTGACG GAGCCCGGGG AGGTGGCGCG TGGGAAGAAG AACGGCCTGG      780
ACTACCTCTT CCATCTCTAC GACCAAGTGC GCGACTTCCT CCTCCAAGTC CAATCCTTGG      840
CCAAGGAGCG GGGCGAGAAA TGCCCCACCA AGGTCCTCCG CCTCTCTTCT TTTTATAGTC      900
TTTCGATACA ATCAAACCTT TTCGAACGTA CCAAGCACG GATCATTCAA ACAAGAAGAC      960
AATGCAG GTG ACG AAC CAG GTG TTC AGG TAC GCG AAG AAG GCG GGA GCA      1009
      Val Thr Asn Gln Val Phe Arg Tyr Ala Lys Lys Ala Gly Ala
      1          5          10
AGC TAC ATA AAC AAG CCG AAG ATG AGG CAC TAT GTC CAC TGC TAC GCC      1057
Ser Tyr Ile Asn Lys Pro Lys Met Arg His Tyr Val His Cys Tyr Ala
      15          20          25          30
CTG CAC TGC CTG GAC GAG CAC GCC TCC AAC GCC CTT CGC AAG AGC TTC      1105
Leu His Cys Leu Asp Glu His Ala Ser Asn Ala Leu Arg Lys Ser Phe
      35          40          45
AAG GAG CGC GGG GAG AAC GTC GGC GCC TGG AGG CAA GCC TGT TAC CAC      1153
Lys Glu Arg Gly Glu Asn Val Gly Ala Trp Arg Gln Ala Cys Tyr His
      50          55          60

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CCC CTG GTC ACC ATC GCC GGC CGC AGG GCC GGC TGG GAC ATC GAC GCC 1201
 Pro Leu Val Thr Ile Ala Gly Arg Arg Ala Gly Trp Asp Ile Asp Ala
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 ATC TTC AAT GCC CAC CCC CGC CTC TGC ATC TGG TAT GTC CCC ACC AAG 1249
 Ile Phe Asn Ala His Pro Arg Leu Cys Ile Trp Tyr Val Pro Thr Lys
 80 85 90
 CTC CGC CAG CTC TGC CAT GCT CAC CGC CAC TCC TCC GCC TCT GCT GCT 1297
 Leu Arg Gln Leu Cys His Ala His Arg His Ser Ser Ala Ser Ala Ala
 95 100 105 110
 TCC TCC GCT TCC ACC TCC ACC TCT GCC CCC ACC GCT CAC CAT CTC GAA 1345
 Ser Ser Ala Ser Thr Ser Thr Ser Ala Pro Thr Ala His His Leu Glu
 115 120 125
 CTC CCT TAC TAGTTCGTGC CCGTTCCTCA TTCTCTTGTC TTTTAGTGTC 1394
 Leu Pro Tyr
 GTATCAGCGC ATGATCATGA GGGAGATGAA AGTACTGTGC TGTGGTCTAT TTCTACTGCA 1454
 ATGAGTATTA ATTGAATTTT AACGTGTAGC TGAGCTGAGC TGAGCT 1500

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Val Thr Asn Gln Val Phe Arg Tyr Ala Lys Lys Ala Gly Ala Ser Tyr
 1 5 10 15
 Ile Asn Lys Pro Lys Met Arg His Tyr Val His Cys Tyr Ala Leu His
 20 25 30
 Cys Leu Asp Glu His Ala Ser Asn Ala Leu Arg Lys Ser Phe Lys Glu
 35 40 45
 Arg Gly Glu Asn Val Gly Ala Trp Arg Gln Ala Cys Tyr His Pro Leu
 50 55 60
 Val Thr Ile Ala Gly Arg Arg Ala Gly Trp Asp Ile Asp Ala Ile Phe
 65 70 75 80
 Asn Ala His Pro Arg Leu Cys Ile Trp Tyr Val Pro Thr Lys Leu Arg
 85 90 95
 Gln Leu Cys His Ala His Arg His Ser Ser Ala Ser Ala Ala Ser Ser
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 Ala Ser Thr Ser Thr Ser Ala Pro Thr Ala His His Leu Glu Leu Pro
 115 120 125
 Tyr

- 29 -

(2) INFORMATION FOR SEQ ID NO.7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 154..906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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CGGCCGCCTC TCTCTCTCTC TCTCTCTCTC TCTCTCTGGT TCAAGAACAC ACCAAAGAAG      60
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GCATCCTCGT CCCCAAGGTT TTTTTCGGGC AGT ATG GAG TTC CCG AGT GAA TTT      174
                               Met Glu Phe Pro Ser Glu Phe
                               1       5
TCA GAG GCC TCT TCA CAG AAG AGA ATC GGG GGG AGA GGG AAA ATA GAG      222
Ser Glu Ala Ser Ser Gln Lys Arg Ile Gly Gly Arg Gly Lys Ile Glu
      10              15              20
ATC AAA CGG ATC GAG AAC ACG ACG AAC CGG CAG GTC ACC TTT TGT AAA      270
Ile Lys Arg Ile Glu Asn Thr Thr Asn Arg Gln Val Thr Phe Cys Lys
      25              30              35
CGC CGG AAC GGG TTG TTG AAG AAG GCT TAT GAG CTA TCG GTG TTG TGC      318
Arg Arg Asn Gly Leu Leu Lys Lys Ala Tyr Glu Leu Ser Val Leu Cys
      40              45              50              55
GAT GCT GAA GTG GCG CTT ATT GTC TTC TCG AGC CGT GGC AGG CTC TAT      366
Asp Ala Glu Val Ala Leu Ile Val Phe Ser Ser Arg Gly Arg Leu Tyr
      60              65              70
GAA TAT GCT AAC AAC AGT GTC AGA GGA ACA ATT GAG AGG TAC AAG AAA      414
Glu Tyr Ala Asn Asn Ser Val Arg Gly Thr Ile Glu Arg Tyr Lys Lys
      75              80              85
GCA AGC AGT GAT TCC TCA CAT CCA CAG TCC GTT TCT GAA GTG AAC ACT      462
Ala Ser Ser Asp Ser Ser His Pro Gln Ser Val Ser Glu Val Asn Thr
      90              95              100
CAG TTT TAT CAG CAA GAA GCA TCC AAG CTT CGG AGA CAG ATA AGA GAA      510
Gln Phe Tyr Gln Gln Glu Ala Ser Lys Leu Arg Arg Gln Ile Arg Glu
      105              110              115
ATC CAG GTC TCA AAT AGG CAT ATT CTA GGT GAG GGT ATA AGT GAT TTG      558
Ile Gln Val Ser Asn Arg His Ile Leu Gly Glu Gly Ile Ser Asp Leu
      120              125              130              135
AGC TTC AAG GAT CTC AAG AAT CTC GAG AGC AAA TTA GAG AAA TCG ATC      606
Ser Phe Lys Asp Leu Lys Asn Leu Glu Ser Lys Leu Glu Lys Ser Ile
      140              145              150
AGC CGA GTT AGA TCA AAG AAG AAT GAG ATG CTT TTT GCC GAG ATT GAG      654
Ser Arg Val Arg Ser Lys Lys Asn Glu Met Leu Phe Ala Glu Ile Glu
      155              160              165

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TAC ATG CAG AAG AGG GAA ATT GAG CTG CAA AAT GAT AAC ATG TAT CTG Tyr Met Gln Lys Arg Glu Ile Glu Leu Gln Asn Asf Asn Met Tyr Leu 170 175 180	702
AGA GCA AAG ATA GCT GAG AAC GAG AGA CCA CAA CAG CAG CAG CAA Arg Ala Lys Ile Ala Glu Asn Glu Arg Ala Gln Gln Gln Gln Gln 185 190 195	750
GGG AGT GAT CAT CAC TTC AAC ATG CCG GGA TCG TCG TCG GTG TAC GAG Gly Ser Asp His His Phe Asn Met Pro Gly Ser Ser Ser Val Tyr Glu 200 205 210 215	798
GCG CTG CCG TCT CAG CCT GCA TAC GAT CGC AAC TTC CTG CAA GTC AAT Ala Leu Pro Ser Gln Pro Ala Tyr Asp Arg Asn Phe Leu Gln Val Asn 220 225 230	846
GTC CTG GAA CCA AAT CAC CAA TCT TAT TCT CGA TCC GAC CAC ACT GCC Val Leu Glu Pro Asn His Gln Ser Tyr Ser Arg Ser Asp His Thr Ala 235 240 245	894
CTC CAA CTC GTC TAATTAAAGC TCAGTTAATA TGTAGCACTA GCAACTGGAC Leu Gln Leu Val 250	946
GTATTGGCAC TCTAGATTAT GCTTTTAAAT ATGCTAGAGT TAGTTGAAAG AGGAATCAAT	1006
GAAGTGGGGA GAGACCCGCA TGATGAGTTT CGCCTAAACA GTGGAAGAAC TCTCTGATAT	1066
TTCTCTTCAT CACTCTTCAA ACTCTTCTGA TGAATCGTGT TGTACAAGGG TTATTGCAAT	1126
TTTTA TAG TACTTAA	1143

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 251 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Glu Phe Pro Ser Glu Phe Ser Glu Ala Ser Ser Gln Lys Arg Ile 1 5 10 15
Gly Gly Arg Gly Lys Ile Glu Ile Lys Arg Ile Glu Asn Thr Thr Asn 20 25 30
Arg Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala 35 40 45
Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Ile Val Phe 50 55 60
Ser Ser Arg Gly Arg Leu Tyr Glu Tyr Ala Asn Asn Ser Val Arg Gly 65 70 75 80
Thr Ile Glu Arg Tyr Lys Lys Ala Ser Ser Asp Ser Ser His Pro Gln 85 90 95

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Ser Val Ser Glu Val Asn Thr Gln Phe Tyr Gln Gln Glu Ala Ser Lys
 100 105 110

Leu Arg Arg Gln Ile Arg Glu Ile Gln Val Ser Asn Arg His Ile Leu
 115 120 125

Gly Glu Gly Ile Ser Asp Leu Ser Phe Lys Asp Leu Lys Asn Leu Glu
 130 135 140

Ser Lys Leu Glu Lys Ser Ile Ser Arg Val Arg Ser Lys Lys Asn Glu
 145 150 155 160

Met Leu Phe Ala Glu Ile Glu Tyr Met Gln Lys Arg Glu Ile Glu Leu
 165 170 175

Gln Asn Asp Asn Met Tyr Leu Arg Ala Lys Ile Ala Glu Asn Glu Arg
 180 185 190

Ala Gln Gln Gln Gln Gln Gly Ser Asp His His Phe Asn Met Pro
 195 200 205

Gly Ser Ser Ser Val Tyr Glu Ala Leu Pro Ser Gln Pro Ala Tyr Asp
 210 215 220

Arg Asn Phe Leu Gln Val Asn Val Leu Glu Pro Asn His Gln Ser Tyr
 225 230 235 240

Ser Arg Ser Asp His Thr Ala Leu Gln Leu Val
 245 250

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1084 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 107..838

(xi) SEQUENCE DESCRIPTION: SEQ ID NC:9:

TAACGCCCA TCTCTTCT CTCTCTCT CTCTCTGTGG CTTGTCTTT TCTTTTGTTT 60

CTTGCCGTTT TGGCGTGTGT GTTGGGTTGT GTGAATTGGA GCGAGG ATG GGG AGG 115
 Met Gly Arg
 1

GGG AGG CTG CAG CTG AAG AGG ATA GAG AAC AAG ATC AAC CGA CAA GTC 163
 Gly Arg Leu Gln Leu Lys Arg Ile Glu Asn Lys Ile Asn Arg Gln Val
 5 10 15

ACC TTC TCC AAG AGG AGG GCG GGT CTG CTC AAG AAG GCC CAC GAG ATC 211
 Thr Phe Ser Lys Arg Arg Ala Gly Leu Leu Lys Lys Ala His Glu Ile
 20 25 30 35

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TCC GTC CTC TGC GAC GCC GAG GTC GCC CTC ATC GTC TTC TCC GCC AAG Ser Val Leu Cys Asp Ala Glu Val Ala Leu Ile Val Phe Ser Ala Lys	259
40 45 50	
GGC AAG CTC TTC GAG TAC TCC ACC GAT TCC TGC ATG GAG AGA ATT CTC Gly Lys Leu Phe Glu Tyr Ser Thr Asp Ser Cys Met Glu Arg Ile Leu	307
55 60 65	
GAA CGC TAT GAA AGA TAC TCA TAT GCG GAG CAC CAA GTT CTT GCA AGC Glu Arg Tyr Glu Arg Tyr Ser Tyr Ala Glu His Gln Val Leu Ala Ser	355
70 75 80	
GAG ACG GAA TCG ATT GGT AGC TGG ACT TTG GAG CAT GCT AAG CTC AAG Glu Thr Glu Ser Ile Gly Ser Trp Thr Leu Glu His Ala Lys Leu Lys	403
85 90 95	
GCC AGA CTT GAA GTT TTA CAC AGA AAT TAT AGG CAT TTC ATG GGC GAA Ala Arg Leu Glu Val Leu His Arg Asn Tyr Arg His Phe Met Gly Glu	451
100 105 110 115	
GAT CTT GAT TCT TTG AGT CTC AAG GAC CTC CAA AAT TTG GAG CAG CAA Asp Leu Asp Ser Leu Ser Leu Lys Asp Leu Gln Asn Leu Glu Gln Gln	499
120 125 130	
CTG GAG TCT GCT CTT AAA CAC ATA AGA TCG AGA AAG AAT CAG CTC ATG Leu Glu Ser Ala Leu Lys His Ile Arg Ser Arg Lys Asn Gln Leu Met	547
135 140 145	
CAT GAA TCA ATC TCA GTG ATT CAG AAA AAG GAT AGG GCA TTG CAG GAG His Glu Ser Ile Ser Val Ile Gln Lys Lys Asp Arg Ala Leu Gln Glu	595
150 155 160	
CAA AAT AAC CTG CTT ACA AAG AAA ATA AAG GAG AAG GAG AGG GCA CTA Gln Asn Asn Leu Leu Thr Lys Lys Ile Lys Glu Lys Glu Arg Ala Leu	643
165 170 175	
GCA CAG CAA GCT CAG TGG GAG CAG CAA GAC CAT GCC CTT GAC TCA CCT Ala Gln Gln Ala Gln Trp Glu Gln Gln Asp His Ala Leu Asp Ser Pro	691
180 185 190 195	
GTT GTT CTA CCC CAC TAC TTG CCA TCT CTC GAC ATC AAT GGC TCT TAT Val Val Leu Pro His Tyr Leu Pro Ser Leu Asp Ile Asn Gly Ser Tyr	739
200 205 210	
CAA GCG AGA CAC AAC GGA CAC GAT GAC GGA GAG AAC CTG ACT CAG CCT Gln Ala Arg His Asn Gly His Asp Asp Gly Glu Asn Leu Thr Gln Pro	787
215 220 225	
CGG GCT GGT ACA CTT CTT CCT CCG TGG ATC TCT GCA TCT CAA TTA AGG Arg Ala Gly Thr Leu Leu Pro Pro Trp Ile Ser Ala Ser Gln Leu Arg	835
230 235 240	
CTT TGACATAAAA GGGAACCTTCT GCTGCTATAT CTTTGATAAG CAATTCTGAA Leu	888
GTCAAGTGAT GAATTGCATG GCATAATCTC AGGCTCTCCC CCACCCTTGT TCTAGCGAAA	948
TAAACATGTC CCTGCTTTTT GCTGCATTCA GTACTCCTAA GTGTGGTCCT CCGTGTATGT	1008
ATAGCACCAT TGCAAATATG CATACCAATG TACATGTATG CAAAATTATA TATGGAAGTT	1068
AACACAACCA TAAAAA	1084

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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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Met Gly Arg Gly Arg Leu Gln Leu Lys Arg Ile Glu Asn Lys Ile Asn
 1           5           10           15
Arg Gln Val Thr Phe Ser Lys Arg Arg Ala Gly Leu Leu Lys Lys Ala
          20           25           30
His Glu Ile Ser Val Leu Cys Asp Ala Glu Val Ala Leu Ile Val Phe
          35           40           45
Ser Ala Lys Gly Lys Leu Phe Glu Tyr Ser Thr Asp Ser Cys Met Glu
          50           55           60
Arg Ile Leu Glu Arg Tyr Glu Arg Tyr Ser Tyr Ala Glu His Gln Val
          65           70           75           80
Leu Ala Ser Glu Thr Glu Ser Ile Gly Ser Trp Thr Leu Glu His Ala
          85           90           95
Lys Leu Lys Ala Arg Leu Glu Val Leu His Arg Asn Tyr Arg His Phe
          100          105          110
Met Gly Glu Asp Leu Asp Ser Leu Ser Leu Lys Asp Leu Gln Asn Leu
          115          120          125
Glu Gln Gln Leu Glu Ser Ala Leu Lys His Ile Arg Ser Arg Lys Asn
          130          135          140
Gln Leu Met His Glu Ser Ile Ser Val Ile Gln Lys Lys Asp Arg Ala
          145          150          155          160
Leu Gln Glu Gln Asn Asn Leu Leu Thr Lys Lys Ile Lys Glu Lys Glu
          165          170          175
Arg Ala Leu Ala Gln Gln Ala Gln Trp Glu Gln Gln Asp His Ala Leu
          180          185          190
Asp Ser Pro Val Val Leu Pro His Tyr Leu Pro Ser Leu Asp Ile Asn
          195          200          205
Gly Ser Tyr Gln Ala Arg His Asn Gly His Asp Asp Gly Glu Asn Leu
          210          215          220
Thr Gln Pro Arg Ala Gly Thr Leu Leu Pro Pro Trp Ile Ser Ala Ser
          225          230          235          240
Gln Leu Arg Leu

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(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1032 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 184..799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCGAACAGTT CAGAAAGACG GATAGATACA TACACAGAGA CATCGATTGC ATCATCTTCT	60
CTACCTCATT GTGCGTGCGG TCGGTGCGGT GCGIGCTTTA TATAGACGCT CGCTCTTACG	120
TTGTTCTCGT CCGCCCGGTG GTGTGGTGGT TGGAGAGAGA GGGAGAGAGA GTAGAGAGAG	180
AAA ATG GGG AGG GGG AGG GTG CAG CTG AAG AGG ATA GAG AAC AAG ATA	228
Met Gly Arg Gly Arg Val Gln Leu Lys Arg Ile Glu Asn Lys Ile	
1 5 10 15	
AAC AGG CAA GTG ACG TTC TCG AAG CGG AGA TGC GGG CTG CTG AAG AAG	276
Asn Arg Gln Val Thr Phe Ser Lys Arg Arg Cys Gly Leu Leu Lys Lys	
20 25 30	
GCC CAC GAG ATC TCC GTC CTC TGC GAC GCC GAC GTC GCC CTC ATC GTC	324
Ala His Glu Ile Ser Val Leu Cys Asp Ala Asp Val Ala Leu Ile Val	
35 40 45	
TTC TCC ACC AAG GGC AAG CTC TTC GAG TAC GCC ACC GAC TGT TGC ATG	372
Phe Ser Thr Lys Gly Lys Leu Phe Glu Tyr Ala Thr Asp Cys Cys Met	
50 55 60	
GAG AGG ATC CTC GAG CGT TAT GAG AGA TAT TCA TAT GCA GAG AGC CAG	420
Glu Arg Ile Leu Glu Arg Tyr Glu Arg Tyr Ser Tyr Ala Glu Ser Gln	
65 70 75	
GTT CTC ACA AAC AAT GCC GAA ACC AAT GGG AAC TGG ACT TTG GAA CAT	468
Val Leu Thr Asn Asn Ala Glu Thr Asn Gly Asn Trp Thr Leu Glu His	
80 85 90 95	
GCA AAA CTC AAG GCC AGG ATG GAG ATT CTG CAG AAA AAT CAA AAG AAT	516
Ala Lys Leu Lys Ala Arg Met Glu Ile Leu Gln Lys Asn Gln Lys Asn	
100 105 110	
CTG ATG GGA GAA GAA CTC GAT TCT CTA AGC CTC AAA GAG CTT CAG AAT	564
Leu Met Gly Glu Glu Leu Asp Ser Leu Ser Leu Lys Glu Leu Gln Asn	
115 120 125	
TTG GAG CAT CAG CTT GAC ACT GCT CTT AAG AAC ATT CGG TCT AGA AAG	612
Leu Glu His Gln Leu Asp Thr Ala Leu Lys Asn Ile Arg Ser Arg Lys	
130 135 140	
ATT CAA CTC ATG TGT GAA TCC ATC TCT GAG CTT CAG AGA AAG GAT AAG	660
Ile Gln Leu Met Cys Glu Ser Ile Ser Glu Leu Gln Arg Lys Asp Lys	
145 150 155	
GCG CTG CAA GAA CAA AAC AAC ATG CTG GCA AAG AAG GTG AAA GAG AAG	708
Ala Leu Gln Glu Gln Asn Met Leu Ala Lys Lys Val Lys Glu Lys	
160 165 170 175	

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GAG AAG GCA CTG GCA CAG CAA ACT CAA TGG GAC AAC CCG CAA GAT GAT 756
 Glu Lys Ala Leu Ala Gln Gln Thr Gln Trp Asp Asn Pro Gln Asp Asp
 180 185 190

GGC CTC ACC TCT TCC TCG GGG TCC TTA CCA TCC GAG TGG AAT T 799
 Gly Leu Thr Ser Ser Ser Gly Ser Leu Pro Ser Glu Trp Asn
 195 200 205

GAGGAGGGAG CGGCCCTCGG TCCACCTCAA CATCGTAATG CCACCCTTTT TCCTTCATGG 859
 ATGCTTAGCC ACCTCCAAGC CTAATTGTCC AATTTATTTG CATGGGAACC ATATATCATT 919
 ACCAATATTA TCTAATGCTT CTTATCGTAT ATATCCAGTC GATATGTAAC CATAATGTAA 979
 CATGTCTTAG TACATGCATT GTGGGGATAC TTGCAAAAAC CTTGTTTTGT AGG 1032

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Gly Arg Gly Arg Val Gln Leu Lys Arg Ile Glu Asn Lys Ile Asn
 1 5 10 15

Arg Gln Val Thr Phe Ser Lys Arg Arg Cys Gly Leu Leu Lys Lys Ala
 20 25 30

His Glu Ile Ser Val Leu Cys Asp Ala Asp Val Ala Leu Ile Val Phe
 35 40 45

Ser Thr Lys Gly Lys Leu Phe Glu Tyr Ala Thr Asp Cys Cys Met Glu
 50 55 60

Arg Ile Leu Glu Arg Tyr Glu Arg Tyr Ser Tyr Ala Glu Ser Gln Val
 65 70 75 80

Leu Thr Asn Asn Ala Glu Thr Asn Gly Asn Trp Thr Leu Glu His Ala
 85 90 95

Lys Leu Lys Ala Arg Met Glu Ile Leu Gln Lys Asn Gln Lys Asn Leu
 100 105 110

Met Gly Glu Glu Leu Asp Ser Leu Ser Leu Lys Glu Leu Gln Asn Leu
 115 120 125

Glu His Gln Leu Asp Thr Ala Leu Lys Asn Ile Arg Ser Arg Lys Ile
 130 135 140

Gln Leu Met Cys Glu Ser Ile Ser Glu Leu Gln Arg Lys Asp Lys Ala
 145 150 155 160

Leu Gln Glu Gln Asn Asn Met Leu Ala Lys Lys Val Lys Glu Lys Glu
 165 170 175

Lys Ala Leu Ala Gln Gln Thr Gln Trp Asp Asn Pro Gln Asp Asp Gly
 180 185 190

Leu Thr Ser Ser Ser Gly Ser Leu Pro Ser Glu Trp Asn
 195 200 205

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(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1070 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 184..920

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TCGAACAGTT CAGAAAGACG GATAGATACA TACACAGAGA CATCGATTGC ATCATCTTCT	60
CTACCTCATT GTGCGTGCGG TCGTGCGGT GCGTGCTTTA TATAGACGCT CGCTCTTACG	120
TTGTTCTCGT CCGCCCGGTG GTGTGGTGGT TGGAGAGAGA GGGAGAGAGA GTAGAGAGAG	180
AAA ATG GGG AGG GGG AGG GTG CAG CTG AAG AGG ATA GAG AAC AAG ATA	228
Met Gly Arg Gly Val Gln Leu Lys Arg Ile Glu Asn Lys Ile	
1 5 10 15	
AAC AGG CAA GTG ACG TTC TCG AAG CGG AGA TGC GGG CTG CTG AAG AAG	276
Asn Arg Gln Val Thr Phe Ser Lys Arg Arg Cys Gly Leu Leu Lys Lys	
20 25 30	
GCC CAC GAG ATC TCC GTC CTC TGC GAC GCC GAC GTC GCC CTC ATC GTC	324
Ala His Glu Ile Ser Val Leu Cys Asp Ala Asp Val Ala Leu Ile Val	
35 40 45	
TTC TCC ACC AAG GGC AAG CTC TTC GAG TAC GCC ACC GAC TGT TGC ATG	372
Phe Ser Thr Lys Gly Lys Leu Phe Glu Tyr Ala Thr Asp Cys Cys Met	
50 55 60	
GAG AGG ATC CTC GAG CGT TAT GAG AGA TAT TCA TAT GCA GAG AGC CAG	420
Glu Arg Ile Leu Glu Arg Tyr Glu Arg Tyr Ser Tyr Ala Glu Ser Gln	
65 70 75	
GTT CTC ACA AAC AAT GCC GAA ACC AAT GGG AAC TGG ACT TTG GAA CAT	468
Val Leu Thr Asn Asn Ala Glu Thr Asn Gly Asn Trp Thr Leu Glu His	
80 85 90 95	
GCA AAA CTC AAG GCC AGG ATG GAG ATT CTG CAG AAA AAT CAA AAG AAT	516
Ala Lys Leu Lys Ala Arg Met Glu Ile Leu Gln Lys Asn Gln Lys Asn	
100 105 110	
CTG ATG GGA GAA GAA CTC GAT TCT CTA AGC CTC AAA GAG CTT CAG AAT	564
Leu Met Gly Glu Glu Leu Asp Ser Leu Ser Leu Lys Glu Leu Gln Asn	
115 120 125	
TTG GAG CAT CAG CTT GAC ACT GCT CTT AAG AAC ATT CGG TCT AGA AAG	612
Leu Glu His Gln Leu Asp Thr Ala Leu Lys Asn Ile Arg Ser Arg Lys	
130 135 140	
ATT CAA CTC ATG TGT GAA TCC ATC TCT GAG CTT CAG AGA AAG GAT AAG	660
Ile Gln Leu Met Cys Glu Ser Ile Ser Glu Leu Gln Arg Lys Asp Lys	
145 150 155	
GCG CTG CAA GAA CAA AAC AAC ATG CTG GCA AAG AAG GTG AAA GAG AAG	708
Ala Leu Gln Glu Gln Asn Met Leu Ala Lys Lys Val Lys Glu Lys	
160 165 170 175	

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GAG AAG GCA CTG GCA CAG CAA ACT CAA TGG GAC AAC CCG CAA GAT GAT 756
 Glu Lys Ala Leu Ala Gln Gln Thr Gln Trp Asp Asn Pro Gln Asp Asp
 180 185 190

GGC CTC ACC TCT TCC TCG GTT ATT CTC TCT CAA TCT TTG CAG CCT CTC 804
 Gly Leu Thr Ser Ser Ser Val Ile Leu Ser Gln Ser Leu Gln Pro Leu
 195 200 205

AAC ATT GGG GGT CCT TAC CAT CCG AGT GGA ATT GAG GAG GGA GCG GCC 852
 Asn Ile Gly Gly Pro Tyr His Pro Ser Gly Ile Glu Glu Gly Ala Ala
 210 215 220

CTC GGT CCA CCT CAA CAT CGT AAT GCC ACC CTT TTT CCT TCA TGG ATG 900
 Leu Gly Pro Pro Gln His Arg Asn Ala Thr Leu Phe Pro Ser Trp Met
 225 230 235

CTT AGC CAC CTC CAA GAA TA ATGATCCAAT TTATTTGCAT GGGAACCATA 950
 Leu Ser His Leu Gln Glu
 240 245

TATCATTACC AATATTATCT AATGCTTCTT ATCGTATATA TCCAGTCGAT ATGTAACCAT 1010
 AATGTAACAT GTCTTAGTAC ATGCATTGTG GGGATACTTG CAAAAACCTT GTTTGTAGG 1070

(2) INFORMATION FOR SEQ ID NO:14:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 245 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Gly Arg Gly Arg Val Gln Leu Lys Arg Ile Glu Asn Lys Ile Asn
 1 5 10 15

Arg Gln Val Thr Phe Ser Lys Arg Arg Cys Gly Leu Leu Lys Lys Ala
 20 25 30

His Glu Ile Ser Val Leu Cys Asp Ala Asp Val Ala Leu Ile Val Phe
 35 40 45

Ser Thr Lys Gly Lys Leu Phe Glu Tyr Ala Thr Asp Cys Cys Met Glu
 50 55 60

Arg Ile Leu Glu Arg Tyr Glu Arg Tyr Ser Tyr Ala Glu Ser Gln Val
 65 70 75 80

Leu Thr Asn Asn Ala Glu Thr Asn Gly Asn Trp Thr Leu Glu His Ala
 85 90 95

Lys Leu Lys Ala Arg Met Glu Ile Leu Gln Lys Asn Gln Lys Asn Leu
 100 105 110

Met Gly Glu Glu Leu Asp Ser Leu Ser Leu Lys Glu Leu Gln Asn Leu
 115 120 125

Glu His Gln Leu Asp Thr Ala Leu Lys Asn Ile Arg Ser Arg Lys Ile
 130 135 140

Gln Leu Met Cys Glu Ser Ile Ser Glu Leu Gln Arg Lys Asp Lys Ala
 145 150 155 160

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Leu	Gln	Glu	Gln	Asn	Asn	Met	Leu	Ala	Lys	Lys	Val	Lys	Glu	Lys	Glu	
				165					170					175		
Lys	Ala	Leu	Ala	Gln	Gln	Thr	Gln	Trp	Asp	Asn	Pro	Gln	Asp	Asp	Gly	
				180					185					190		
Leu	Thr	Ser	Ser	Ser	Val	Ile	Leu	Ser	Gln	Ser	Leu	Gln	Pro	Leu	Asn	
		195					200					205				
Ile	Gly	Gly	Pro	Tyr	His	Pro	Ser	Gly	Ile	Glu	Glu	Gly	Ala	Ala	Leu	
		210					215					220				
Gly	Pro	Pro	Gln	His	Arg	Asn	Ala	Thr	Leu	Phe	Pro	Ser	Trp	Met	Leu	
		225					230					235				
Ser	His	Leu	Gln	Glu												
					245											

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 997 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 38..724

(xi) SEQUENCE DESCRIPTION: SEO ID NO:15:

GCTTCCATCT CCAGGGAAGA GTTTGAACT TGC	GACC ATG GGT TTT CCA ACC CAA	55
	Met Val Phe Pro Thr Gln	
	1 5	
GCC ACG CCC GAG GAG TCC CCG CAG AGG AAA ATG GGG AGG GGA AAG ATC	103	
Ala Thr Pro Glu Glu Ser Pro Gln Arg Lys Met Gly Arg Gly Lys Ile		
10 15 20		
GAG ATC AAG CGG ATC GAG AAC ACG ACG AAT CGG CAA GTG ACT TTC TGC	151	
Glu Ile Lys Arg Ile Glu Asn Thr Thr Asn Arg Gln Val Thr Phe Cys		
25 30 35		
AAG CGG CGG AAT GGC CTC CTC AAG AAG GCA TAT GAA CTC TCC GTT CTT	199	
Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala Tyr Glu Leu Ser Val Leu		
40 45 50		
TGC GAA CGC GAG GTC GCC CTC ATC GTC TTC TCC AGC CGC GGT CGC CTC	247	
Cys Glu Arg Glu Val Ala Leu Ile Val Phe Ser Ser Arg Gly Arg Leu		
55 60 65 70		
TAT GAG TAT GCC AAC GAT AGT GTC AAA GCA ACC ATC GAG AGG TAC AAG	295	
T, Glu Tyr Ala Asn Asp Ser Val Lys Ala Thr Ile Glu Arg Tyr Lys		
75 80 85		
AAG GCT TTC TCA GAT TCC TCC AGT AGC GGG ATC CGT TCT GAA GCT AAT	343	
Lys Ala Phe Ser Asp Ser Ser Ser Ser Gly Ile Arg Ser Glu Ala Asn		
90 95 100		
GTT CAG TTT TAT CAG CAA GAA TCC GCA AAG TTG CAA CAA CAG ATT AAT	391	
Val Gln Phe Tyr Gln Gln Glu Ser Ala Lys Leu Gln Gln Ile Asn		
105 110 115		

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AAC ATG CAG AAC AAT AAC AGG CAA CTG GTG GGT GAC TCA ATT GCT GGG Asn Met Gln Asn Asn Asn Arg Gln Leu Val Gly Asp Ser Ile Ala Gly 120 125 130	439
ATG AAT ATG AAG GAT ATG AAG ACT ACG GAG CAA AAA CTA GAA AAA GCA Met Asn Met Lys Asp Met Lys Thr Thr Glu Gln Lys Leu Glu Lys Ala 135 140 145 150	487
ATC GCT AAA ATT CGC GCC AAA AAG AAT GAG CTT CTA TTT GCG GAG ATT Ile Ala Lys Ile Arg Ala Lys Lys Asn Glu Leu Leu Phe Ala Glu Ile 155 160 165	535
GAG TAT ATG CAA AAA AGG GAA ATT GAC CTA CAC AAC AAC AAT CAA GTT Glu Tyr Met Gln Lys Arg Glu Ile Asp Leu His Asn Asn Asn Gln Val 170 175 180	583
CTG CGA GCG AAG ATC GCG GAG AGC GAG AGG TCC CAA CAT GCG GAT ATG Leu Arg Ala Lys Ile Ala Glu Ser Glu Arg Ser Gln His Ala Asp Met 185 190 195	631
AAT TTG ATG CCG GGA GGT ACC AAC TAT GAC TTC ATG CAG CCA TCT TCT Asn Leu Met Pro Gly Gly Thr Asn Tyr Asp Phe Met Glr Pro Ser Ser 200 205 210	679
TCT CAG CCT TTT GAT TCC AGA AAC TAC TTC CAA GTG AAC GTG CTG Ser Gln Pro Phe Asp Ser Arg Asn Tyr Phe Gln Val Asn Val Leu 215 220 225	724
TAGCACCCAA CCACTGTGAG TGTGCACAAG TCTAGTATCG ATTGAAGGGA ATATAACTAG	784
TATATGGAGC TTCTAAGTGC TTATTATGAG GTTATGATGG ACTTCATCAG ATGTTAATTA	844
AGTAGAAGCA GTTGGCAGAT GCATCTATTA GGTGAAGGGC GTCCTCATCC TTTTGTGAT	904
TAGCATCCTT AGATGTCTTA AAATTTCCAC CATCTTTGTT AAGGTGTGTA TTTGGGTCCC	964
TATGTACTAA ACTGAATATG AACTATCGAA CTA	997

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Val Phe Pro Thr Gln Ala Thr Pro Glu Glu Ser Pro Gln Arg Lys 1 5 10 15
Met Gly Arg Gly Lys Ile Glu Ile Lys Arg Ile Glu Asn Thr Thr Asn 20 25 30
Arg Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala 35 40 45
Tyr Glu Leu Ser Val Leu Cys Glu Arg Glu Val Ala Leu Ile Val Phe 50 55 60
Ser Ser Arg Gly Arg Leu Tyr Glu Tyr Ala Asn Asp Ser Val Lys Ala 65 70 75 80

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[illegible]

THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. An isolated nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding a product or derivative thereof required for normal flower development in a woody perennial.
2. An isolated nucleic acid molecule according to claim 1 wherein the woody perennial is a species of the genus *Eucalyptus*.
3. An isolated nucleic acid molecule according to claim 1 or 2 wherein the species of *Eucalyptus* is selected from *Eucalyptus alpina*, *Eucalyptus annulata*, *Eucalyptus astringens*, *Eucalyptus behriana*, *Eucalyptus benthamii*, *Eucalyptus botryoides*, *Eucalyptus brockwayi*, *Eucalyptus caesia*, *Eucalyptus calophylla* 'Rosea', *Eucalyptus calycogona*, *Eucalyptus camaldulensis*, *Eucalyptus camaldulensis* ssp. *subcinerea*, *Eucalyptus campaspe*, *Eucalyptus camphora*, *Eucalyptus citriodora*, *Eucalyptus cladocalyx*, *Eucalyptus cladocalyx* 'Nana', *Eucalyptus cloeziana*, *Eucalyptus cornuta*, *Eucalyptus cosmophylla*, *Eucalyptus crenulata*, *Eucalyptus crucis*, *Eucalyptus delegatensis*, *Eucalyptus desmondensis*, *Eucalyptus dielsii*, *Eucalyptus diptera*, *Eucalyptus diversicolor*, *Eucalyptus diversifolia*, *Eucalyptus dumosa*, *Eucalyptus dundasii*, *Eucalyptus dunnii*, *Eucalyptus eremophila*, *Eucalyptus erythrocorys*, *Eucalyptus erythronema*, *Eucalyptus ficifolia*, *Eucalyptus flocktoniae*, *Eucalyptus foecunda*, *Eucalyptus forrestiana*, *Eucalyptus gardneri*, *Eucalyptus gillii*, *Eucalyptus globulus*, *Eucalyptus globulus* ssp. *globulus*, *Eucalyptus globulus* ssp. *pseudoglobulus*, *Eucalyptus globulus* ssp. *maidenii*, *Eucalyptus globulus* ssp. *bicostata*, *Eucalyptus gomphocephala*, *Eucalyptus gracilis*, *Eucalyptus grandis*, *Eucalyptus griffithsii*, *Eucalyptus grossa*, *Eucalyptus henrii*, *Eucalyptus increassata*, *Eucalyptus kitsoniana*, *Eucalyptus kondininensis*, *Eucalyptus kruseana*, *Eucalyptus lansdowneana*, *Eucalyptus largiflorens*, *Eucalyptus lehmanni*, *Eucalyptus leucoxylon*, *Eucalyptus leucoxylon* (Pink) (syn. 'Rosea'), *Eucalyptus lesouefii*, *Eucalyptus macrandra*, *Eucalyptus macrocarpa*, *Eucalyptus maculata*, *Eucalyptus marginata*, *Eucalyptus melliodora*, *Eucalyptus microcarpa*, *Eucalyptus nicholii*, *Eucalyptus nitens*, *Eucalyptus nutans*, *Eucalyptus obliqua*, *Eucalyptus occidentalis*, *Eucalyptus ochrophloia*, *Eucalyptus oleosa*, *Eucalyptus*

orbifolia, *Eucalyptus ovata*, *Eucalyptus pauciflora*, *Eucalyptus parvifolia*, *Eucalyptus perriniana*, *Eucalyptus pileata*, *Eucalyptus pellita*, *Eucalyptus pilularis*, *Eucalyptus platypus*, *Eucalyptus polyanthemos*, *Eucalyptus porosa*, *Eucalyptus preissiana*, *Eucalyptus pyriformis*, *Eucalyptus regnans*, *Eucalyptus resinifera*, *Eucalyptus rhodantha*, *Eucalyptus robusta*, *Eucalyptus saligna*, *Eucalyptus salmonophloia*, *Eucalyptus salubris*, *Eucalyptus sargentii*, *Eucalyptus sepulcralis*, *Eucalyptus sideroxylon* 'Rosea', *Eucalyptus sieberi*, *Eucalyptus spathulata*, *Eucalyptus socialis*, *Eucalyptus steedmanii*, *Eucalyptus stoatei*, *Eucalyptus stricklandii*, *Eucalyptus tereticornis*, *Eucalyptus tetragona*, *Eucalyptus tetraptera*, *Eucalyptus torquata*, *Eucalyptus* 'Torwood', *Eucalyptus urnigera*, *Eucalyptus urophylla*, *Eucalyptus viminalis*, *Eucalyptus viridis*, *Eucalyptus wandoo*, *Eucalyptus websteriana*, *Eucalyptus woodwardii*.

4. An isolate nucleic acid molecule according to any one of claims 1 to 3, wherein the species of *Eucalyptus* is *Eucalyptus benthamii*, *Eucalyptus botryoides*, *Eucalyptus camaldulensis*, *Eucalyptus citriodora*, *Eucalyptus cloeziana*, *Eucalyptus delegatensis*, *Eucalyptus diversicolor*, *Eucalyptus dunnii*, *Eucalyptus globulus*, *Eucalyptus globulus subspecies bicostata*, *Eucalyptus globulus subspecies globulus*, *Eucalyptus globulus subspecies maidenii*, *Eucalyptus globulus subspecies pseudoglobulus*, *Eucalyptus grandis*, *Eucalyptus henrii*, *Eucalyptus maculata*, *Eucalyptus marginata*, *Eucalyptus nitens*, *Eucalyptus obliqua*, *Eucalyptus pellita*, *Eucalyptus pilularis*, *Eucalyptus regnans*, *Eucalyptus resinifera*, *Eucalyptus saligna*, *Eucalyptus sieberi*, *Eucalyptus tereticornis*, *Eucalyptus urophylla*, *Eucalyptus viminalis*.

5. An isolated nucleic acid molecule according to any one of claims 1 to 4 wherein the species of *Eucalyptus* is *Eucalyptus globulus ssp globulus* or *Eucalyptus nitens*.

6. An isolated nucleic acid molecule according to any one of claims 1 to 5 wherein the nucleic acid is DNA.

7. An isolated nucleic acid molecule according to any one of claims 1 to 6 wherein the nucleotide sequence corresponds to a gene selected from leafy (*LFY*), apetala 1 (*API*) or agamous (*AG*) from *Arabidopsis* or floricaula (*FLO*), squamosa (*SQUA*) or

plena from *Antirrhium* (*PLE*).

8. An isolated nucleic acid molecule according to any one of claims 1 to 7 wherein the nucleic acid molecule is selected from the following:
 - (i) comprises a nucleotide sequence set forth in SEQ ID NO:1 or 3 or 5 and is analogous to *LFY* and/or *FLO*;
 - (ii) comprises a nucleotide sequence set forth in SEQ ID NO:9 or 11 or 13 and is analogous to *API* and/or *SQUA*; or
 - (iii) comprises a nucleotide sequence set forth in SEQ ID NO:7 or 15 and is analogous to *AG* and/or *PLE*.
9. An isolated DNA molecule of eucalypt origin encoding a reproductive gene and which is capable of hybridising under low stringency conditions to a nucleic acid molecule having a nucleotide sequence as set forth in or complementary to SEQ ID NO:1 or 3 or 5.
10. An isolated DNA molecule of eucalypt origin encoding a reproductive gene and which is capable of hybridising under low stringency conditions to a nucleic acid molecule having a nucleotide sequence as set forth in or complementary to SEQ ID NO:9 or 11 or 13.
11. An isolated DNA molecule of eucalypt origin encoding a reproductive gene and which is capable of hybridising under low stringency conditions to a nucleic acid molecule having a nucleotide sequence as set forth in or complementary to SEQ ID NO:7 or 15.
12. A method of minimising inflorescence in a woody perennial, said method comprising introducing into one or more cells of said wood perennial a genetic construct capable of down-regulating or up-regulating expression of a reproductive gene in said woody perennial, regenerating a transgenic plant from said one or more cells and growing said plant for a time and under conditions sufficient to permit expression of said genetic construct.

13. A method according to claim 12 wherein the woody perennial is a species of the genus *Eucalyptus*.

14. A method according to claim 13 wherein the species of *Eucalyptus* is selected from *Eucalyptus alpina*, *Eucalyptus annulata*, *Eucalyptus astringens*, *Eucalyptus behriana*, *Eucalyptus benthamii*, *Eucalyptus botryoides*, *Eucalyptus brockwayi*, *Eucalyptus caesia*, *Eucalyptus calophylla* 'Rosea', *Eucalyptus calycogona*, *Eucalyptus camaldulensis*, *Eucalyptus camaldulensis* ssp. *subcinerea*, *Eucalyptus campaspe*, *Eucalyptus camphora*, *Eucalyptus citriodora*, *Eucalyptus cladocalyx*, *Eucalyptus cladocalyx* 'Nana', *Eucalyptus cloeziana*, *Eucalyptus cornuta*, *Eucalyptus cosmophylla*, *Eucalyptus crenulata*, *Eucalyptus crucis*, *Eucalyptus delegatensis*, *Eucalyptus desmondensis*, *Eucalyptus dielsii*, *Eucalyptus diptera*, *Eucalyptus diversicolor*, *Eucalyptus diversifolia*, *Eucalyptus dumosa*, *Eucalyptus dundasii*, *Eucalyptus dunnii*, *Eucalyptus eremophila*, *Eucalyptus erythrocorys*, *Eucalyptus erythronema*, *Eucalyptus ficifolia*, *Eucalyptus flocktoniae*, *Eucalyptus foecunda*, *Eucalyptus forrestiana*, *Eucalyptus gardneri*, *Eucalyptus gillii*, *Eucalyptus globulus*, *Eucalyptus globulus* ssp. *globulus*, *Eucalyptus globulus* ssp. *pseudoglobulus*, *Eucalyptus globulus* ssp. *maidenii*, *Eucalyptus globulus* ssp. *bicostata*, *Eucalyptus gomphocephala*, *Eucalyptus gracilis*, *Eucalyptus grandis*, *Eucalyptus griffithsii*, *Eucalyptus grossa*, *Eucalyptus henrii*, *Eucalyptus increassata*, *Eucalyptus kitsoniana*, *Eucalyptus kondininensis*, *Eucalyptus kruseana*, *Eucalyptus lansdowneana*, *Eucalyptus largiflorens*, *Eucalyptus lehmanni*, *Eucalyptus leucoxylon*, *Eucalyptus leucoxylon* (Pink) (syn. 'Rosea'), *Eucalyptus lesouefii*, *Eucalyptus macrandra*, *Eucalyptus macrocarpa*, *Eucalyptus maculata*, *Eucalyptus marginata*, *Eucalyptus melliodora*, *Eucalyptus microcarpa*, *Eucalyptus nicholii*, *Eucalyptus nitens*, *Eucalyptus nutans*, *Eucalyptus obliqua*, *Eucalyptus occidentalis*, *Eucalyptus ochrophloia*, *Eucalyptus oleosa*, *Eucalyptus orbifolia*, *Eucalyptus ovata*, *Eucalyptus pauciflora*, *Eucalyptus parvifolia*, *Eucalyptus perriniana*, *Eucalyptus pileata*, *Eucalyptus pellita*, *Eucalyptus pilularis*, *Eucalyptus platypus*, *Eucalyptus polyanthemus*, *Eucalyptus porosa*, *Eucalyptus preissiana*, *Eucalyptus pyriformis*, *Eucalyptus regnans*, *Eucalyptus resinifera*, *Eucalyptus rhodantha*, *Eucalyptus robusta*, *Eucalyptus saligna*, *Eucalyptus salmonophloia*, *Eucalyptus salubris*, *Eucalyptus sargentii*, *Eucalyptus sepulcralis*, *Eucalyptus sideroxylon* 'Rosea', *Eucalyptus sieberi*, *Eucalyptus spathulata*, *Eucalyptus*

socialis, *Eucalyptus steedmanii*, *Eucalyptus stoatei*, *Eucalyptus stricklandii*, *Eucalyptus tereticornis*, *Eucalyptus tetragona*, *Eucalyptus tetraptera*, *Eucalyptus torquata*, *Eucalyptus 'Torwood'*, *Eucalyptus urnigera*, *Eucalyptus urophylla*, *Eucalyptus viminalis*, *Eucalyptus viridis*, *Eucalyptus wandoo*, *Eucalyptus websteriana*, *Eucalyptus woodwardii*.

15. A method according to claim 14 wherein the species of *Eucalyptus* is selected from *Eucalyptus benthamii*, *Eucalyptus botryoides*, *Eucalyptus camaldulensis*, *Eucalyptus citriodora*, *Eucalyptus cloeziana*, *Eucalyptus delegatensis*, *Eucalyptus diversicolor*, *Eucalyptus dunnii*, *Eucalyptus globulus*, *Eucalyptus globulus subspecies bicostata*, *Eucalyptus globulus subspecies globulus*, *Eucalyptus globulus subspecies maidenii*, *Eucalyptus globulus subspecies pseudoglobulus*, *Eucalyptus grandis*, *Eucalyptus henrii*, *Eucalyptus maculata*, *Eucalyptus marginata*, *Eucalyptus nitens*, *Eucalyptus obliqua*, *Eucalyptus pellita*, *Eucalyptus pilularis*, *Eucalyptus regnans*, *Eucalyptus resinifera*, *Eucalyptus saligna*, *Eucalyptus sieberi*, *Eucalyptus tereticornis*, *Eucalyptus urophylla*, *Eucalyptus viminalis*.

16. A method according to any one of claims 12 to 15 wherein the species of *Eucalyptus* is *Eucalyptus globulus ssp globulus* or *Eucalyptus nitens*.

17. A method according to any one of claims 12 to 16 wherein the reproductive gene corresponds to one or more of SEQ ID NO:1 or 3 or 5, SEQ ID NO:9 or 11 or 13 and/or SEQ ID NO:7 or 15.

18. A method according to any one of claims 12 to 17 wherein the resulting plant is substantially sterile.

19. A transgenic woody perennial plant which exhibits a substantial reduction in reproductive capability.

20. A transgenic plant according to claim 19 wherein said plant is substantially sterile.

21. A transgenic plant according to claim 19 or 20 wherein said wood perennial is a species of *Eucalyptus*.

22. A transgenic plant according to claim 21 wherein the species of *Eucalyptus* is selected from *Eucalyptus alpina*, *Eucalyptus annulata*, *Eucalyptus asringens*, *Eucalyptus behriana*, *Eucalyptus benthamii*, *Eucalyptus botryoides*, *Eucalyptus brockwayi*, *Eucalyptus caesia*, *Eucalyptus calophylla* 'Rosea', *Eucalyptus calycogona*, *Eucalyptus camaldulensis*, *Eucalyptus camaldulensis* ssp. *subcinerea*, *Eucalyptus campaspe*, *Eucalyptus camphora*, *Eucalyptus citriodora*, *Eucalyptus cladocalyx*, *Eucalyptus cladocalyx* 'Nana', *Eucalyptus cloeziana*, *Eucalyptus cornuta*, *Eucalyptus cosmophylla*, *Eucalyptus crenulata*, *Eucalyptus crucis*, *Eucalyptus delegatensis*, *Eucalyptus desmondensis*, *Eucalyptus dielsii*, *Eucalyptus diptera*, *Eucalyptus diversicolor*, *Eucalyptus diversifolia*, *Eucalyptus dumosa*, *Eucalyptus dundasii*, *Eucalyptus dunnii*, *Eucalyptus eremophila*, *Eucalyptus erythrocorys*, *Eucalyptus erythronema*, *Eucalyptus ficifolia*, *Eucalyptus flocktoniae*, *Eucalyptus foecunda*, *Eucalyptus forrestiana*, *Eucalyptus gardneri*, *Eucalyptus gillii*, *Eucalyptus globulus*, *Eucalyptus globulus* ssp. *globulus*, *Eucalyptus globulus* ssp. *pseudoglobulus*, *Eucalyptus globulus* ssp. *maidenii*, *Eucalyptus globulus* ssp. *bicostata*, *Eucalyptus gomphocephala*, *Eucalyptus gracilis*, *Eucalyptus grandis*, *Eucalyptus griffithsii*, *Eucalyptus grossu*, *Eucalyptus henrii*, *Eucalyptus increassata*, *Eucalyptus kitsoniana*, *Eucalyptus kondininensis*, *Eucalyptus kruseana*, *Eucalyptus lansdowneana*, *Eucalyptus largiflorens*, *Eucalyptus lehmanni*, *Eucalyptus leucoxylon*, *Eucalyptus leucoxylon* (Pink) (syn. 'Rosea'), *Eucalyptus lesouefii*, *Eucalyptus macrandra*, *Eucalyptus macrocarpa*, *Eucalyptus maculata*, *Eucalyptus marginata*, *Eucalyptus melliodora*, *Eucalyptus microcarpa*, *Eucalyptus nicholii*, *Eucalyptus nitens*, *Eucalyptus nutans*, *Eucalyptus obliqua*, *Eucalyptus occidentalis*, *Eucalyptus ochrophloia*, *Eucalyptus oleosa*, *Eucalyptus orbifolia*, *Eucalyptus ovata*, *Eucalyptus pauciflora*, *Eucalyptus parvifolia*, *Eucalyptus perriniana*, *Eucalyptus pileata*, *Eucalyptus pellita*, *Eucalyptus pilularis*, *Eucalyptus platypus*, *Eucalyptus polyanthemos*, *Eucalyptus porosa*, *Eucalyptus preissiana*, *Eucalyptus pyriformis*, *Eucalyptus regnans*, *Eucalyptus resinifera*, *Eucalyptus rhodantha*, *Eucalyptus robusta*, *Eucalyptus saligna*, *Eucalyptus salmonophloia*, *Eucalyptus salubris*, *Eucalyptus sargentii*, *Eucalyptus sepulcralis*, *Eucalyptus sideroxylon* 'Rosea', *Eucalyptus sieberi*, *Eucalyptus spathulata*, *Eucalyptus*

socialis, *Eucalyptus steedmanii*, *Eucalyptus stoatei*, *Eucalyptus stricklandii*, *Eucalyptus tereticornis*, *Eucalyptus tetragona*, *Eucalyptus tetraptera*, *Eucalyptus torquata*, *Eucalyptus 'Torwood'*, *Eucalyptus urnigera*, *Eucalyptus urophylla*, *Eucalyptus viminalis*, *Eucalyptus viridis*, *Eucalyptus wandoo*, *Eucalyptus websteriana*, *Eucalyptus woodwardii*.

23. A transgenic plant according to claim 22 wherein the species of *Eucalyptus* is selected from *Eucalyptus benthamii*, *Eucalyptus botryoides*, *Eucalyptus camaldulensis*, *Eucalyptus citriodora*, *Eucalyptus cloeziana*, *Eucalyptus delegatensis*, *Eucalyptus diversicolor*, *Eucalyptus dunnii*, *Eucalyptus globulus*, *Eucalyptus globulus subspecies bicostata*, *Eucalyptus globulus subspecies globulus*, *Eucalyptus globulus subspecies maidenii*, *Eucalyptus globulus subspecies pseudoglobulus*, *Eucalyptus grandis*, *Eucalyptus henrii*, *Eucalyptus maculata*, *Eucalyptus marginata*, *Eucalyptus nitens*, *Eucalyptus obliqua*, *Eucalyptus pellita*, *Eucalyptus pilularis*, *Eucalyptus regnans*, *Eucalyptus resinifera*, *Eucalyptus saligna*, *Eucalyptus sieberi*, *Eucalyptus tereticornis*, *Eucalyptus urophylla*, *Eucalyptus viminalis*.

24. A transgenic plant according to any one of claims 19 to 23 wherein the species of *Eucalyptus* is *Eucalyptus globulus ssp globulus* or *Eucalyptus nitens*.

25. A method for identifying a gene required for normal flower development in a woody perennial, said method comprising isolating a nucleic acid molecule from said wood perennial and cloning a region of said nucleic acid molecule having at least 45% nucleotide similarity to all or a region of *Arabiopsis* genes *LFY*, *AP1* or *AG* or *Antirrhinium* genes *FLO*, *SQUA* or *PLE*.

26. A method according to claim 25 wherein the woody perennial is a species of the genus *Eucalyptus*.

27. A method according to claim 26 wherein the species of *Eucalyptus* is selected from *Eucalyptus alpina*, *Eucalyptus annulata*, *Eucalyptus astringens*, *Eucalyptus behriana*, *Eucalyptus benthamii*, *Eucalyptus botryoides*, *Eucalyptus brockwayi*, *Eucalyptus caesia*, *Eucalyptus calophylla 'Rosea'*, *Eucalyptus calycogona*, *Eucalyptus*

camaldulensis, *Eucalyptus camaldulensis* ssp. *subcinerea*, *Eucalyptus campaspe*,
Eucalyptus camphora, *Eucalyptus citriodora*, *Eucalyptus cladocalyx*, *Eucalyptus*
cladocalyx 'Nana', *Eucalyptus cloeziana*, *Eucalyptus cornuta*, *Eucalyptus cosmophylla*,
Eucalyptus crenulata, *Eucalyptus crucis*, *Eucalyptus delegatensis*, *Eucalyptus*
desmondensis, *Eucalyptus dielsii*, *Eucalyptus diptera*, *Eucalyptus diversicolor*, *Eucalyptus*
diversifolia, *Eucalyptus dumosa*, *Eucalyptus dundasii*, *Eucalyptus dunnii*, *Eucalyptus*
eremophila, *Eucalyptus erythrocorys*, *Eucalyptus erythronema*, *Eucalyptus ficifolia*,
Eucalyptus flocktoniae, *Eucalyptus foecunda*, *Eucalyptus forrestiana*, *Eucalyptus*
gardneri, *Eucalyptus gillii*, *Eucalyptus globulus*, *Eucalyptus globulus* ssp. *globulus*,
Eucalyptus globulus ssp. *pseudoglobulus*, *Eucalyptus globulus* ssp. *maidenii*, *Eucalyptus*
globulus ssp. *bicostata*, *Eucalyptus gomphocephala*, *Eucalyptus gracilis*, *Eucalyptus*
grandis, *Eucalyptus griffithsii*, *Eucalyptus grossa*, *Eucalyptus henrii*, *Eucalyptus*
increassata, *Eucalyptus kitsoniana*, *Eucalyptus kondininensis*, *Eucalyptus kruseana*,
Eucalyptus lansdowneana, *Eucalyptus largiflorens*, *Eucalyptus lehmanni*, *Eucalyptus*
leucoxylon, *Eucalyptus leucoxylon* (Pink) (syn. 'Rosea'), *Eucalyptus lesouefii*, *Eucalyptus*
macrandra, *Eucalyptus macrocarpa*, *Eucalyptus maculata*, *Eucalyptus marginata*,
Eucalyptus melliodora, *Eucalyptus microcarpa*, *Eucalyptus nicholii*, *Eucalyptus nitens*,
Eucalyptus nutans, *Eucalyptus obliqua*, *Eucalyptus occidentalis*, *Eucalyptus ochrophloia*,
Eucalyptus oleosa, *Eucalyptus orbifolia*, *Eucalyptus ovata*, *Eucalyptus pauciflora*,
Eucalyptus parvifolia, *Eucalyptus perriniana*, *Eucalyptus pileata*, *Eucalyptus pellita*,
Eucalyptus pilularis, *Eucalyptus platypus*, *Eucalyptus polyanthemus*, *Eucalyptus porosa*,
Eucalyptus preissiana, *Eucalyptus pyriformis*, *Eucalyptus regnans*, *Eucalyptus resinifera*,
Eucalyptus rhodantha, *Eucalyptus robusta*, *Eucalyptus saligna*, *Eucalyptus*
salmonophloia, *Eucalyptus salubris*, *Eucalyptus sargentii*, *Eucalyptus sepulcralis*,
Eucalyptus sideroxylon 'Rosea', *Eucalyptus sieberi*, *Eucalyptus spathulata*, *Eucalyptus*
socialis, *Eucalyptus steedmanii*, *Eucalyptus stoatei*, *Eucalyptus stricklandii*, *Eucalyptus*
tereticornis, *Eucalyptus tetragona*, *Eucalyptus tetraptera*, *Eucalyptus torquata*,
Eucalyptus 'Torwood', *Eucalyptus urnigera*, *Eucalyptus urophylla*, *Eucalyptus viminalis*,
Eucalyptus viridis, *Eucalyptus wandoo*, *Eucalyptus websteriana*, *Eucalyptus woodwardii*.

28. A method according to claim 27 wherein the species of *Eucalyptus* is selected from *Eucalyptus benthamii*, *Eucalyptus botryoides*, *Eucalyptus camaldulensis*, *Eucalyptus citriodora*, *Eucalyptus cloeziana*, *Eucalyptus delegatensis*, *Eucalyptus diversicolor*, *Eucalyptus dunnii*, *Eucalyptus globulus*, *Eucalyptus globulus subspecies bicostata*, *Eucalyptus globulus subspecies globulus*, *Eucalyptus globulus subspecies maidenii*, *Eucalyptus globulus subspecies pseudoglobulus*, *Eucalyptus grandis*, *Eucalyptus henrii*, *Eucalyptus maculata*, *Eucalyptus marginata*, *Eucalyptus nitens*, *Eucalyptus obliqua*, *Eucalyptus pellita*, *Eucalyptus pilularis*, *Eucalyptus regnans*, *Eucalyptus resinifera*, *Eucalyptus saligna*, *Eucalyptus sieberi*, *Eucalyptus tereticornis*, *Eucalyptus urophylla*, *Eucalyptus viminalis*.

29. A method according to any one of claims 25 to 28 wherein the species of *Eucalyptus* is *Eucalyptus globulus ssp globulus* or *Eucalyptus nitens*.

30. An isolated nucleic acid molecule according to any one of claims 1 to 11 or a method according to any one of claims 12 to 18 or a transgenic woody perennial according to any one of claims 19 to 24 or a method according to any one of claims 25 to 29 substantially as hereinbefore described with reference to the Figures and/or Examples.

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COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH
ORGANISATION

By Its Patent Attorneys

DAVIES COLLISON CAVE

ABSTRACT

The present invention relates generally to plants and more particularly to woody perennial plants such as eucalypts with reduced reproductive capacity. The present invention is also directed to genetic constructs useful in the generation of woody perennial plants with reduced reproductive capacity. The present invention is most particularly directed to sterile trees of the genus *Eucalyptus* which are useful in the establishment of wood lot plantations, in re-forestation projects and in developing modified eucalyptus trees with beneficial properties.

-120 CCACTACGTACGTACATACACTGTACATTGAATATACTAAACACATGGACCCATGTGTTT
 -60 ATAAAACAAGGAAGCCAGACTCCTGTACCCTTACACGCTGAAGCCATTTGAAGCCGGAGA
 0 ATGGATCCAGAAGCATTGCGGTTGTGGGTTGCCAACGATCGGGGACTCGAGGAGCTG
 0 M D P E A F A V V G L R T M G G L E E L
 61 TTCGAGGCTTATGGCATAAGGTACCTCAGGCTCCAGGATAGCGGAAATGGGTTTACG
 21 F E A Y G I R Y L T A S R I A E M G F T
 121 GCCAACACCTCCTCGACATGAAGGAGGAGCTCGACCACATGATGAACCTCCCTCTCC
 41 A N T L L D M K E E E L D D M M N S L S
 181 CACATCTTCGCTGGGACCTCCTCGTCGGCGAGCGCTACGGCATCAAGGCCGCCATCCGC
 61 H I F R W D L L V G E R Y G I K A A I R
 241 GCCGAGCGCGGACGCTCCTCGAAGCGGATACCGCGCGCCACCACCTCCACTCCACCCAC
 81 A E R R R L L E A D D R R H H L H S T D
 301 CATGCCCTCCTCGATGCTCTCTCCACCAAGGTACCTTAGCTCGGCCTCTTTGATTTTTG
 101 H A L L D A L S H Q G
 361 ACGTTTTGGGTCAATTATGATTATCCCACGAGGCTGTGGAGGAACAAGTGGTGCAGC
 112 L S E E Q V V Q H
 421 ACTCAGACAAGGATCAGCTGGGCAGGCGGGAAGCGGGACACGGCGGGCAGCTCGTGGG
 121 S E K D Q L G R A G S G D T A G T S W G
 481 CGGCCAACAACAGAGAAAGAAGCATCGTCATCGTCACCACATCACCGGATGAAAGGAG
 141 A Q Q Q R K K H R H R H H I T A M K G A
 641 CGGCCACGGAAGAGGACGAGGAGGAGGAGGAGGAAGTGGAGGAGATGAGGAGCCAGAGGG
 161 A T E E D E E D E E E V E E M R R Q R E
 701 AGCACCCCTTCATAGTGACGGAGCCCGGGGAGGTGGCGCGTGGGAAGAACAACGGCCTGG
 181 H P F I V T E P G E V A R G K K N G L D
 761 ACTACCTCTTCCATCTCTACGACCAGTGGCGGACTTCTCTCTCCAAGTCCAATCCTTGG
 201 Y L F H L Y D Q C R D F L L Q V Q S L A
 821 CCAAGGAGCGCGGGGAGAAATGCCCCACCAAGGTCTCCGCTCTCTCTTTTATAGTC
 221 K E R G E K C P T K
 881 TTTGATACAATCAAACCTTCTTGAACGTACCCAAGCACGGATCATTCAAACAAGAAGAC
 941 AATGCACGTGACGAACCAGGTGTTTACGGTACGCGAAGAAGCGGGAGCAAGCTACATAAA
 231 V T N Q V F R Y A K K A G A S Y I N
 1001 CAAGCCGAAGATGAGGCACTATGTCCACTGCTACGCCCTGCACTGCCTGGACGAGCACGG
 249 K P K M R H Y V H C Y A L H C L D E H A
 LFY-309-H
 1061 CTCCAACGCCCTTCGCAAGAGCTTCAAGGAGCGCGGGGACAACGTCGGCGCCTGGAGGCA
 269 S N A L R K S F K E R G E N V G A W R Q
 1121 AGCCTGTTACCACCCCTGGTCACCATCGCGCGCGCAGGGCGGCTGGGACATCGACGC
 289 A C Y H P L V T I A G R R A G W D I D A
 LFY-351-J
 1181 CATCTTCAATGCCACCCCGGCTCTGCATCTGGTATGTCCCCACCAAGCTCCGCCAGCT
 309 I F N A H P R L C I W Y V P T K L R Q L
 1241 CTGCCATGCTCAGCGGCACTCCTCGGCTCTGCTGCTTCTCGGCTTCCACCTCCACCTC
 329 C H A H R H S S A S A A S S A S T S T S
 1301 TGCCCCACCGCTCACCATCTCCAACCTCCCTTACTAGTTCGTGCCCCGTTCCTCATTCTCT
 349 A P T A H H L E L P Y stop 359
 1361 TGTGTTTTAGTGTCGTATCACCGCATGATCATGAGGGACATGAAAGTACTGTGCTGTGGT
 1441 CTATTTCTACTGCAATCAGTATTAATTGAATTTTAACGTGTAGCTGAGCTGAGCTGAGCT

FIGURE 1

FIGURE 2

FIGURE 4

tcgaacagttcagaaagacggatagatacatcacagagacatcgattgcatcatcttct
ctacctcattgtgctgctgctgctgctgctgctgctttatatagacgctcgtctcttacg
ttgttctcgtccgccccggtggtgtggtggttggagagagagggagagagagtagagagag
aaaATGGGGAGGGGGAGGGTGCAGCTGAAGAGGATAGAGAACAAGATAAACAGGCAAGTG
M G R G R V Q L K R I E N K I N R Q V
ACGTTCTCGAAGCGGAGATGCGGGCTGCTGAAGAAGGCCACGAGATCTCCGTCCTCTGCG
T F S K R R C G L L K K A H E I S V L C
GACGCCGACGTCGCCCTCATCGTCTTCTCCACCAAGGGCAAGCTCTTCGAGTACGCCACC
D A D V A L I V F S T K G K L F E Y A T
GACTGTTGCATGGAGAGGATCCTCGAGCGTTATGAGAGATATTCATATGCAGAGAGCCAG
D C C M E R I L E R Y E R Y S Y A E S Q
GTTCTCACAAACAATGCCGAAACCAATGGGAACTGGACTTTGGAACATGCAAACTCAAG
V L T N N A E T N G N W T L E H A K L K
GCCAGGATGGAGATTCTGCAGAAAAATCAAAAGAATCTGATGGGAGAAGAAGCTCGATTCT
A R M E I L Q K N Q K N L M G E E L D S
CTAAGCCTCAAAGAGCTTCAGAATTTGGAGCATCAGCTTGACACTGCTCTTAAGAACATT
L S L K E L Q N L E H Q L D T A L K N I
CGGTCTAGAAAGATTCAACTCATGTGTGAATCCATCTCTGAGCTTCAGAGAAAGGATAAG
R S R K I Q L M C E S I S E L Q R K D K
GCGCTGCAAGAACAACAACATGCTGGCAAAGAAGGTGAAAGAGAAGGAGAAGGCACTG
A L Q E Q N N M L A K K V K E K E K A L
GCACAGCAAACCTCAATGGGACAACCCGCAAGATGATGGCCTCACCTCTTCCTCGGGGTCC
A Q Q T Q W D N P Q D D G L T S S S G S
TTACCATCCGAGTGGAATTGAggagggagcggccctcggtccacctcaacatcgtaatgc
L P S E W N *
caccctttttccttcatggatgcttagccacctccaagcctaattgtccaattttatttgc
atgggaaccatatatcattaccaatattatctaagcttcttatcgatatatccagtcg
atatgtaaccataatgtaacatgtcttagtacatgcattgtggggataacttgcaaaaacc
ttgtttttagg

FIGURE 5

tcgaacagttcagaaagacggatagatacacagagacatcgattgcatcatcttct
ctacctcattgtgctgcggtgctgctgctgtgctttatatagagctcgtctctacg
ttgttctcgtccgccccggtggtgtggtggttggagagagagggagagagagtagagagag
aaaATGGGGAGGGGAGGGTGCAGCTGAAGAGGATAGAGAACAAGATAAACAGGCAAGTG
M G R G R V Q L K R I E N K I N R Q V
ACGTTCTCGAAGCGGAGATGCGGGCTGCTGAAGAAGGCCACGAGATCTCCGTCCTCTGC
T F S K R R C G L L K K A H E I S V L C
GACGCCGACGTCGCCCTCATCGTCTTCTCCACCAAGGGCAAGCTCTTCGAGTACGCCACC
D A D V A L I V F S T R G K L F E Y A T
GACTGTTGCATGGAGAGGATCCTCGAGCGTTATGAGAGATATTCATATGCAGAGAGCCAG
D C C M E R I L E R Y E R Y S Y A E S Q
GTTCTCACAACAATGCCGAAACCAATGGGAAGTGGACTTTGGAACATGCAAACTCAAG
V L T N N A E T N G N W T L E H A K L K
GCCAGGATGGAGATTCTGCAGAAAAATCAAAAGAATCTGATGGGAGAAGAACTCGATTCT
A R M E I L Q K N Q K N L M G E E L D S
CTAAGCCTCAAAGAGCTTCAGAATTTGGAGCATCAGCTTGACACTGCTCTTAAGAACATT
L S L K E L Q N L E H Q L D T A L K N I
CGGTCTAGAAAGATTCAACTCATGTGTGAATCCATCTCTGAGCTTCAGAGAAAGGATAAG
R S R K I Q L M C E S I S E L Q R K D K
GCGCTGCAAGAACAACAACATGCTGGCAAAGAAGGTGAAAGAGAAGGAGAAGGCACTG
A L Q E Q N N M L A K K V K E K E K A L
GCACAGCAAACCTCAATGGGACAACCCGCAAGATGATGGCCTCACCTCTTCCTCGGTTATT
A Q Q T Q W D N P Q D D G L T S S S V I
CTCTCTCAATCTTTGCAGCCTCTCAACATTGGGGGTCTTACCATCCGAGTGAATTGAG
L S Q S L Q P L N I G G P Y H P S G I E
GAGGGAGCGGCCCTCGGTCCACCTCAACATCGTAATGCCACCCTTTTTCCTTCATGGATG
E G A A L G P P Q H R N A T L F P S W M
CTTAGCCACCTCCAAGAATAatgatccaatttatttgcattggaaccatatatcattacc
L S H L Q E *
aatattatctaattgcttcttatcgtatatatccagtcgatatgtaaccataatgtaacat
gtcttagtacatgcattgtggggatacttgcaaaaaccttgttttgtagg

FIGURE 6

GGAATTCGCG GCCGCTGAAA GGGCATTTCGT TTCATTAATT CATGTCTCCG CTCATCTCAA	60
CTCGAACAGT TCAGAAAGAC AGATAGATAC ATACACAGAG ACATCGATTG CATCATCTTC	120
TCTACCTCAT TGTGCTGGG GTGCGTGCGG TGCCTGCTTT ATATAGACGC TCGCTCTTAC	180
GTTGTTCTCG TCCGCCCGGT GGTGTGGTGG TTGGAGAGAG AGGGAGAGAG AGTAGAGAGA	240
GAAA ATG GGG AGG GGG AGG GTG CAG CTC AAG AGG ATA GAG AAC AAG ATA Met Gly Arg Gly Arg Val Gln Leu Lys Arg Ile Glu Asn Lys Ile	289
1 5 10 15	
AAC AGG CAA GTG ACG TTC TCG AAG CGG AGA TGC GGG CTG CTG AAG AAG Asn Arg Gln Val Thr Phe Ser Lys Arg Cys Gly Leu Leu Lys Lys	337
20 25 30	
GCC CAC GAG ATC TCC GTC CTC TGC GAC GCC GAC GTC GCC CTC ATC GTC Ala His Glu Ile Ser Val Leu Cys Asp Ala Asp Val Ala Leu Ile Val	385
35 40 45	
TTC TCC ACC AAG GGC AAG CTC TTC GAG TAC GCC ACC GAC TGT TGC ATG Phe Ser Thr Lys Gly Lys Leu Phe Glu Tyr Ala Thr Asp Cys Cys Met	433
50 55 60	
GAG AGG ATC CTC GAG CGT TAT GAG AGA TAT TCA TAT GCA GAG AGC CAG Glu Arg Ile Leu Glu Arg Tyr Glu Arg Tyr Ser Tyr Ala Glu Ser Gln	481
65 70 75	
GTT CTC ACA AAC AAT GCC GAA ACC AAT GGG AAC TGG ACT TTG GAA CAT Val Leu Thr Asn Asn Ala Glu Thr Asn Gly Asn Trp Thr Leu Glu His	529
80 85 90 95	
GCA AAA CTC AAG GCC AGG ATG GAG ATT CTG CAG AAA AAT CAA AAG AAT Ala Lys Leu Lys Ala Arg Met Glu Ile Leu Gln Lys Asn Gln Lys Asn	577
100 105 110	
CTG ATG GGA GAA GAA CTC GAT TCT CTA AGC CTC AAA GAG CTT CAG AAT Leu Met Gly Glu Glu Leu Asp Ser Leu Ser Leu Lys Glu Leu Gln Asn	625
115 120 125	
TTG GAG CAT CAG CTT GAC ACT GCT CTT AAG AAC ATT CGG TCT AGA AAG Leu Glu His Gln Leu Asp Thr Ala Leu Lys Asn Ile Arg Ser Arg Lys	673
130 135 140	
ATT CAA CTC ATG TGT GAA TCC ATC TCT GAG CTT CAG AGA AAG GAT AAG Ile Gln Leu Met Cys Glu Ser Ile Ser Glu Leu Gln Arg Lys Asp Lys	721
145 150 155	
GCG CTG CAA GAA CAA AAC AAC ATG CTG GCA AAG AAG GTG AAA GAG AAG Ala Leu Gln Glu Gln Asn Asn Met Leu Ala Lys Lys Val Lys Glu Lys	769
160 165 170 175	
GAG AAG GCA CTG GCA CAG CAA ACT CAA TGG GAC AAC TCG CAA GAT GAT Glu Lys Ala Leu Ala Gln Gln Thr Gln Trp Asp Asn Pro Gln Asp Asp	817
180 185 190	
GGC CTC ACC TCT TCC TCG GGG TCC TTA CCA TCC GAG TGG AAT TGA GGA Gly Leu Thr Ser Ser Ser Gly Ser Leu Pro Ser Glu Trp Asn * Gly	865
195 200 205	
GGG AGC GGC CCT CGG TCC ACC TCA ACA TCG TAA TGC CAC CCT TTT TCC Gly Ser Gly Pro Arg Ser Thr Ser Thr Ser * Cys His Pro Phe Ser	913
210 215 220	
TTC ATG GAT GCT TAG CCA CCT CCA AGA A TAATGATCCA ATTTATTGC Phe Met Asp Ala * Pro Pro Pro Arg	961
225 230	
ATGGGAACCA TATATCATT CCAATATTAT CTAATGCTTC TTATCGTATA TATCAATCG	1021
ATATGTAACC ATAATGTAAC ATGTCTTAGT ACATGCATTG TGGGGATACT TGCAAAAACC	1081
TTGTTTTGTA GG	1093

FIGURE 7

GCTTCCATCT CCAGGGAAGA GTTTGAAC TGC GACC ATG GTT TTT CCA ACC CAA	55
Met Val Phe Pro Thr Gln	
1 5	
GCC ACG CCC GAG GAG TCC CCG CAG AGG AAA ATG GGG AGG GGA AAG ATC	103
Ala Thr Pro Glu Ser Pro Gln Arg Lys Met Gly Arg Gly Lys Ile	
10 15 20	
GAG ATC AAG CGG ATC GAG AAC ACG ACG AAT CGG CAA GTG ACT TTC TGC	151
Glu Ile Lys Arg Ile Glu Asn Thr Thr Asn Arg Gln Val Thr Phe Cys	
25 30 35	
AAG CGG CGG AAT GGC CTC CTC AAG AAG GCA TAT GAA CTC TCC GTT CTT	199
Lys Arg Arg Asn Gly Leu Lys Lys Ala Tyr Glu Leu Ser Val Leu	
40 45 50	
TGC GAA CGC GAG GTC GCC CTC ATC GTC TTC TCC AGC CGC GGT CGC CTC	247
Cys Glu Arg Glu Val Ala Leu Ile Val Phe Ser Ser Arg Gly Arg Leu	
55 60 65 70	
TAT GAG TAT GCC AAC GAT AGT GTC AAA GCA ACC ATC GAG AGG TAC AAG	295
Tyr Glu Tyr Ala Asn Asp Ser Val Lys Ala Thr Ile Glu Arg Tyr Lys	
75 80 85	
AAG GCT TTC TCA GAT TCC TCC AGT AGC GGG ATC CGT TCT GAA GCT AAT	343
Lys Ala Phe Ser Asp Ser Ser Ser Ser Gly Ile Arg Ser Glu Ala Asn	
90 95 100	
GTT CAG TTT TAT CAG CAA GAA TCC GCA AAG TTG CAA CAA CAG ATT AAT	391
Val Gln Phe Tyr Gln Gln Glu Ser Ala Lys Leu Gln Gln Ile Asn	
105 110 115	
AAC ATG CAG AAC AAT AAC AGG CAA CTG GTG GGT GAC TCA ATT GCT GGG	439
Asn Met Gln Asn Asn Asn Arg Gln Leu Val Gly Asp Ser Ile Ala Gly	
120 125 130	
ATG AAT ATG AAG GAT ATG AAG ACT ACG GAG CAA AAA CTA GAA AAA GCA	487
Met Asn Met Lys Asp Met Lys Thr Thr Glu Gln Lys Leu Glu Lys Ala	
135 140 145 150	
ATC GCT AAA ATT CGC GCC AAA AAG AAT GAG CTT CTA TTT GCG GAG ATT	535
Ile Ala Lys Ile Arg Ala Lys Lys Asn Glu Leu Leu Phe Ala Glu Ile	
155 160 165	
GAG TAT ATG CAA AAA AGG GAA ATT GAC CTA CAC AAC AAC AAT CAA GTT	583
Glu Tyr Met Gln Lys Arg Glu Ile Asp Leu His Asn Asn Asn Gln Val	
170 175 180	
CTG CGA GCG AAG ATC GCG GAG AGC GAG AGG TCC CAA CAT GCG GAT ATG	631
Leu Arg Ala Lys Ile Ala Glu Ser Glu Arg Ser Gln His Ala Asp Met	
185 190 195	
AAT TTG ATG CCG GGA GGT ACC AAC TAT GAC TTC ATG CAG CCA TCT TCT	679
Asn Leu Met Pro Gly Gly Thr Asn Tyr Asp Phe Met Gln Pro Ser Ser	
200 205 210	
TCT CAG CCT TTT GAT TCC AGA AAC TAC TTC CAA GTG AAC GTG CTG	724
Ser Gln Pro Phe Asp Ser Arg Asn Tyr Phe Gln Val Asn Val Leu	
215 220 225	
TAGCACCCAA CCACTGTGAG TGTGCACAAG TCTAGTATCG ATTGAAGGGA ATATACTAG	784
TATATGGAGC TTCTAAGTGC TTATTATGAG GTTATGATGG ACTTCATCAG ATGTTAATTA	844
AGTAGAAGCA GTTGGCAGAT GCATCTATTA GGTGAAGGGC CTCCTCATCC TTTTGTGAT	904
TAGCATCCTT AGATGTCTTA AAATTTCCAC CATCTTTGTT AAGGTGTGTA TTTGGGTCCC	964
TATGTACTAA ACTGAATATG AACTATCGAA CTA	997